

FIGURE 1

CCAATCGCCCCGGTGC GGTTGTCAGGGTCTCGGGCTAGTCAATGGGCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
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TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG
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AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTGTGGTGTCAACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTGTTTTATAAAGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCATTCTCTCT
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ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
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FIGURE 2

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NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGGVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGTTGGGCCCCGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCCGACCGCGTGTCTGAGCCCTGGGCACGCGGAACGGGAGGAGTCTGAGGGT
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 GCCGGGTAGGCTCTGGAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCAGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGCT
 GTTCCCTCTTTGCGGGGTCTCACAGAAAGAGGTTCTTGGGGGTGCGCCCTTCTGAGGAGGCT
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 CAGTACCCACTGCTGACACAAGGAGCCAACACGGGACCTGTTGCGCCACCAAGGAGGGGC
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 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGCTGGAATGTCTAAATGTTTC
 TGTAGCAGAAAACACGATAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
 AENSAVPTADTRSQPRDPVRPFRGRGPHEPRKKQNVDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTTGGCC
 CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTTAACGGAAGT
 CAAGAATGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
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 TCTCTTTGCAATCTGGGCTGCGTCTTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
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FIGURE 6

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GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFRRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL
```

Signal peptide:

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amino acids 1-24
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Transmembrane domain:

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amino acids 86-103, 60-75
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Casein kinase II phosphorylation site.

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amino acids 82-86
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Tyrosine kinase phosphorylation site.

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amino acids 144-151
```

N-myristoylation site.

```
amino acids 4-10, 5-11, 47-53, 170-176, 176-182
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Prokaryotic membrane lipoprotein lipid attachment site.

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amino acids 54-65
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G-protein coupled receptors proteins.

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amino acids 44-85
```

FIGURE 7

AATTCAGATTTTAAGCCCATTCCTGCAGTGGAATTTTCATGAAC TAGCAAGAGGACACCATCTT
 CTTGTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT
 GCTAGGCCCTCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAAC TAAAGATTGAAG
 ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTTGAAACTTTGGCAGCC
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 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
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 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA
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FIGURE 8

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AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCC**ATG**CGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTGACGCCGCCAGTGGGCGGGGCCCTTGGGCGCTCGCCACCACT
 GTAGTCATGTACCCACCGCCGCCGCCCGCTCATCGGGACTTCACTTCGGTGACGCTGAG
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 CGCCACGCTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTAGCTGGAGTTCGGG
 GAGCTCTCCCTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA
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 GCCTCTTACCACCACTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
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 GCTCATGGAGACTTGTACAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCAGAGATCG
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FIGURE 10

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IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTEQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLEPSRRAEVPTKPPPLPPARTQGTVPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSVDNIGTGVAHPPRWTSDDSTVAEVTSIQLEFRELRLTGDKKQFEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIIQGGKQETQLLEDYVEAIEGVRT
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AYVFNTAEHPLPIWTPA

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Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**SATG**TTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGGTGCTCTCCGGCGGCCCTCCCTCGGAAGTGTTCCGCTCTCCACCTGTTCTGTGGC
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FIGURE 12

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RHHIYVLNQVDHFRFNRAALINVG FLESSNSTDYIAMHDVDLLPLNEELDYGFP EAGPFHVA
SPELHPLYHYKTYVGGILL LSKQHYRLCNGMSNRFWG WGREDDFYRRIKGAGLQLFRPSGI
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NIMLDCDKTATPWCTFS
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Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

CAATGTTTGCCTATCACACCTCCCCAAGCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCATCAGGGATTGGGCTTCTTCCCCCTTCCTTTCTGTGTCTC
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FIGURE 14

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PRGEGEKVG DG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCACGCGCAGCCGCGAGCGGACAAAG
 GAGCATGTCCGCGCCGGGGAAGGCCCTCTCCGCGCCGCATAGGGTCTCGGTCTCCGCGCTGG
 GCCCGCGCGCGCTCTCTGCCCGCCGGGCTCCGGGCGGCCCTAGGCCAGTGCGCCGCGCG
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 GACTACAGCTGATTGAAGCAAAATAGAGGAGGCACAACTCCAGACCCCTAAAGCAACCACT
 TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTTAATCTCACAG
 TACTTTATTTCTGTCTTGTCCCTCAATAATATCAAAACAATATTCAGTCATTTTAATGGC
 TGCAATAAAGTATGTCACCAAGGTTAGGTGTTCTGTTTGTAGTGTGAGCACTCAATGAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPDTPNRTVTLLSNNKISELKNGSFSGLSLLERLDRNNLISSIDPGA
 FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLSGNLFSSLSQGTFDYLASLRSLFQ
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMT
 SHRQVVFEGDSLPPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGCCHVQTKRGNNTRTVDIVVLESSAQYCPPERVNNKGDFRWPRTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDVMVDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRITGLSDYGRRDPEGNLDKQLSFKCNVSNFTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

FIGURE 17

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
 ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
 CAGAGACATTGAGAGGCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
 TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAA
 TC**ATGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTTGAT
 GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
 AATAAAGGACAGTGGGTCAATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
 GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
 TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
 TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
 TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 19

CTGTGGTATGAAAAAG

FIGURE 20

```

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VQFLSHGRSRDHAI AATFFSCIA CVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQP ALEWC VAVYAICFILAAIAILLNLGECTNVLPPIPPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFKV

```

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

TTAAAGCTGGCAACATGCCCTATTAATTTTGTATTTTATGATAGACAGGGGGTTTACCATGTTGGCCAGCGCTGGTCT
TTAAAGCTGCTGACCTATCATCCGCTCACTCGGCTCCCAAGGTCGTGGGATATACAGGATAGACCATGACGCT
CTGGCCAGCCTCATGATTTTAAAGAAATTATCTGTATTAGTGTCTGTCTAAACATTTGGGCATACAGTACACCA
AAACAGACATGAATTTCCCAAGAGCCAAAGCCAGTGGGAGACCAACACAGAAACAGAAATGCCAAAGACACCA
TTATTACTCACTATGATTAAGGTCACAAATGGGGTACTGTTATGGAGAGTGATTTGTTAAGAGACTACAGAGG
AGGACAGACATACCAAGAGGGGGGCCAGGAAGAGCTCTGATGACAGAGTGTGATTTACGCCCAAACTGGGAAGATGA
GAAGAGAGCTAGCCAGCATCAGATAGTTCTCCAGAGAGAGCTGGGAGAGCTACATCTACATCATTTGGCTGTGAGA
AATAGCATGGGATTTGGAGGAGCTGTGGGGGAACACCACTTTCCGCCAGCTGGGAGAGGAGCATTTAGGGGCTTGA
AAGGGCATGGCAGTACAGTATGAAGAAGACAGGTTAGGAGAGAGGACTTTCCAGTGGGAATGATTAGGTCTTAT
AACGATATAATGGGCACCAAGCCAGGGGAGAAATTTAGTGGTATGCTGAGTTTGGAGCCAGCTAGATGGGACAG
TGTGGGTGATGCCAAAGGAAGAGTACGAAGACGGGCACAGCTGGGGAAGAGTTGTGGGGTTTGGTTTCCA
TCTTCCCGAGTGTCCCGGAATGTGTTGTTGGGAACACAGAGGAGGAGACAGGGGCCAGAGGGGAAGGGAATCTTAA
AGAAGTCTCGATGACACACTCTCTGATTCCTTCCCTCTTCCCTCTCTCAGAGGTCCTACTCGTGGTTCTTCTAT
TTCCTGCCCTGCCCTCACTCTCTGGGTGCTGGAAAGTGGGAATTAGCTGAAGTTTGGCTTCTCGGGGCTCTG
TCTGATATCTCATTTGCTTTGGGAGACATAATCCACTGTCCTAGCTTTCTATCATCTCAATTTCCCTTGAAG
CCAGCTGGGACATATGTTGGTTGCTTCTCTAGCTGTCTCTCTCTCACTGCTTTCTGGGTATGGGATCTGTAG
GGGAGTACTGATTTGCTGTAGGCGGCACACTGACTTTCTAATGCTTACCACAAAGTGAATTTGGAGACAGCTG
CGGATGCTGCCAAGTCCCGCGCGAGCTTAACTATCAGGAGATCGCTGCGCTGGCAGGCTCCCTCGTCAATGCT
ATGACGCCCTTCCAAAGTTTCTGGCCACTTTGCTCTTCTCCGTTTGCAATATCCCTTTGGAACGTGTTTCTGT
GTGATGATACATGCTGGGTTCTCCCTTTCTTCCCTTCTCAGTGAATCTCAGGCCCTTTCCCAACCAAGGCTTCA
CATGGATCTTAACTACTGCCACCTTCCACTTCCCTGCACTGTCTGCTTGGCTGGCTGGTCTTACAGGCTTCA
TCCACCTTCCCTTACTCCAGTATTTCCAGGTGGTGAAGAACCACTGTACCAAGCTTACGCCACTGGCCACAGG
GCCAGTGGCTCACTCTAATGTTGAAGGGCTGGAGACAGCCGAGTACTCACTGTCTGCTGGATCAGCTCT
TTTCTTCTATTACAGCTACGAGAGGCGCAACAGAGGCTCGTTTCCAGCAGAGTGGCTGAGCAGTTTTGGCA
TCCGCGAAGCCAGCTCCGACATGGTCTTCTGTTGAGTGGCAGAGCTACATGATCATCTTATGATGAGTCT
TGTCTGGGGATGGACAGACATGGCTGGGAGCTGCCCTGGGCGGACCTCCAGAGCACTGTTTCAACGCCCC
ACCGGTTCTTCCGGCTCTGTGGCCAGAGCTTGGTGGAGCTGAGACAGCACTCTCAGAGCTGTCCCCAGCA
CCCTGTGCTCTAGCTGTGACAGCTGAGGATGGTTTGGGCTCCCGGCGGCTGCTCTCCAGCTCTGTGG
GCTGATGACTGTTCTGCCAAATCTGCCCCACCGGGGAAGTGTCTTCCGAGCTCTGGGCCCTTGGAGGCC
AGGACTCACTCTAAGCTCGCCCTCAGAGAGTCTGCTTTTCCCGCGGAGGAGGAGCAGCGCCCTCGAAGG
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GGGTGGTCTCTTAGTAGAGTAGGACAGGACAGGAGAAAGCAAGCCCACTATGCTCTGGAGTGGATGCA
TCCCCGGCTCTGCGACGGGCGAGAGCTCTGTGCCAAGTGTGGGCTCAAGGCTCCAGCAGACCTCCACAGCC
TAGAGGCTCTGGGAGGCTCGCTTCTCGGTTGTTTGTAGTAAGTTTGGAGAGGAGCGAGGGGCTG
GGCTCGGCGACATGTCTGCCCACTCCGGGCTTCCGCGGGGCTTCCCGGGGCTCTGGGCTAGGCTACGCTA
GCTGTGGCAGCAGTGATGTTCTATGTTCTTAAATAGGACACACAATTTCTCTCGGTAATGTGAACAACTA
AGGGGTTGTGACTGGGCTGTGAGGCTGGGTTGGGAGGGGCGGACAAACCCCACTCCCTCACTGCTCTCT
TCTTCTGTTCTTTCTACTTCCAGTCACTGTGCAGTGGTATAGTAAGTACACCCCACTGAGGCGGCTG
CTCTCTGCCCTCCGGAGCTCTAAGGTGTAGCGCTCCCTCAAGGGCCCTTGCCAGTGTGGCTGTGCTGTGCTCT
ATTACCTCTCCATCTGTTTAAATTTCTCTTTTCTTAAAGACAGAAAGTTTGGTCTGTGTTTTCATGCT
GGATCTCTCTCTCTGGGAGGCTTTGGAATGATCGGAGTGTACCTTCCACCTTTTCTGGCCCTCTAATGG
GGCTTGGGCTCTTCCCAACCTCTTAGATGTAGGCGAGTGTCTGGCGCTCACAGCGACGGGCTGCC
ATTCAAGCAGAGCTCTCAGCGGGAGGTGAAGAAAGGATGTGCTCTGTTGCAACAGAGCTGGGATCTGATTT
CTTCTAGAGAGGGCCACAGAGGCGACAGGGGTGGCGGGAGTTGTCAGTGTATGCTGCTGCTGACAGGACAGAT
TGTGCCATGAGTGACAGTCTATGGGAGCTTCTCTTCTGGGAGGAAGAAGTATAGGCTTCTGTCTGAAT
GAAAGGCAAGGCTACAGTACAGGCGCCGCGCCGACCTGCTGTTGAATGCCAGCTGTAGTGGAGGCTCTGGCAG
ATCTTGCAATCCAAGTCACTGACTGTACGTTTATGTTTGTGTTGGGAGGTTGGTGGCTTTAGAAATTAAGGG
CTTGATGCTTTGGCAGTTAGGAGGCCCAAGTGAAGACAGAGCCACGGGCAAGCACTTATATATAGT
GGCTATTAGTGTGTTATTTGTTCTATTAAAGATTTGTTTATTAAATTAATATAAAATCTTTGTAATCTCT

FIGURE 22

MFLATLSFLLPFAHFFGTVSCEYMLGSPLSSLAQVNLSPFSSHFKVHMDPNYCHPSTSLHLCS
 LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRFPVRQGSVEFESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE
 LLLAKLPPSRESAFRSLGLEAQDSLNSPLTESCLSPAEEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT
 GGCACCTCCTGCTCAGTGCACATTTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA
 CAGATTCCTTTTCAGACAGGACAACCTGTGATATTTTCAGTTTCCTGATTGTAATACCTCCTAAG
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
 TACAATCTATTCTTTGCCACATCAAGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAAG
 AAGCCTACA**ATGT**TTGGCCTTAGCCAAAATTCTGTTGATTTCACGTTGTTTTATTCACTTCT
 ATCGGGGAGCCATGAAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTTT
 TTAACAACATGAAAAATAAACCTATTCTTTGGAAAGTGAAGCAAACCTTAAACTCAGATAAA
 GAAAAATATAACCACCTCAAATCTCAAGGCGAGTCATCCCCCTCCTTTGAATCTACCCAACAA
 CAGCCACGGAATAACAGATTCTCCAGTAACCTATCAGCAGAGCATTCCTTTGGGCAGTCTAA
 AACCCACATCTACCATTTCCACAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT
 TGGAAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
 TGCTCTGTCTCTCAGAAAATTCACCTTGGTCTTTGGTCAATGACACCGTGAAACCTCCTGATA
 ACAGTTCCATTACAGTTAGCATCCTCTCTCAGAACCAACTTCTCCATCTGTGACCCCCCTG
 ATAGTGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
 TCAAGAAAAAACACTCTACAGCCTACCTTAAAAATTCAACAAATAATTCAAAACCTTTTCCAA
 ATACGTGAGATCCCCAAAAAGAAAATAGAATACAGGAATAGTATTGCGGGCCATTTTAGGT
 GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGAAAAAGGAAAAAC
 GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAAGTTCTGCGATTAGACA
 ATGACCCGGAACCTTATGATGTGAGTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT
 GATTGAGCCATGCCGAAAAGTGAAGAAAATGCACGTGATGGCATTCCTATGGATGACATACC
 TCCACTTCGTACTTCTGTAT**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCTCTA
 CATCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTAAGTGTGACGTGGAT
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTTCTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
 TGTATTTTAGTAGTATTTCTTAGTAGAAAAATTTGTGGAATCAGATAAAACTAAAAAGATT
 TCACCATCAGCCCTGCGCTCATAACTAAATAATAAAAAATTATTCACCAAAAAATTTCTAAA
 ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
 TTTCTTAAATGAAAATGAAAGGGTGCTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
 GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
 TAGTACGTTATAATTTCTAGATCAGCACACATGATCAGCCCATGAGTTATGAAGCTGA
 CAATGACTGCATTTCAACGGGGCCATGGCAGGAAAGCTGACCTACCCAGGAAAGTAATAGCT
 TCTTTAAAGTCTTCAAAGGTTTGGGAATTTAACTTGTCTTAATATATCTTAGGCTTCAA
 TTATTTGGGTGCCTTAAAAACTCAATGAGAATCATGGT

FIGURE 24

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 ><subunit 1 of 1, 334 aa, 1 stop
 ><MW: 36294, pI: 4.98, NX(S/T): 13
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 TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
 PIADEDLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSI LSSEPTSPSVTPLIVE
 PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNPNTSDPQKENRNTGIVFGAILGAIL
 GVSLLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDV SFGNSSYYNPTLNSA
 MP ESEENARDGIPMD DIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
 163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCACTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATGG**TGAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
 TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAATTCTGCTGTGACTGAGGAGGCTGACATTCGTGA
 GGTGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCCTGCAG
 CAATTATTCACTACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGTCTGGGGAAGTGC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGTTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTAGTAACCTTGGCATCTTTATTTACCACTTTGCAATAACAGA
 AAGTCCCTCCGCCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAGGAAAAAAAAAAAAAACTACTAACCACGTCAAGCTCTTGTCAAATTTTAGTTTAAT
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTTCTTGCATTTATAG
 GGTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC
 GTTGTTTTTTTTGTGTTGTTGTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAATTTGAAATATTTAAATTGTTTTTGAACCTTTTGTGTAAATATA
 TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCAATTTGTACAACCTTCTTGATTTAGA
 AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG
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FIGURE 26

```

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IIDVPVPSFSDSDPAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKILASG
RYLPQTYVVREDLVAVEEIRDVSNLGIIFIYQLCNNRKSFRLLRRDLLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCCAGCCCCAGAGCAGCCCCGGGCACCCAGCAGGACTCTCT
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTGCGCGGGAGCACCCAGTCTGTACGCC
 AAGGAAGTGGTCTGGGGGCAC**CATG**GTTTCGGCGGCAGCCCCAGCCTCTCATCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCTGTCTACCGACGCCCCGTCTGTGCCCTGAAGGCCAGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCTCCCCGAGCCTCC
 CGCCACCTTGACCCCGGCCCTCAGCCCCACATCGATGGGGGCCAGCCCCACAACCTGGGG
 GGCCCATCACCCCCACCAACTTCTTGATGGGATAGTGGACTTCTTCGGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGTGTATGTTTCATCGTCTGTGCCGCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCCTCGGCCATTACCCATCGTCTTCCCCAAGAAGAAGTAC
 GTGGACAGAGTGACCGGGCCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCCAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG
 CACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCCGACAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCCAGGAAGTCCA
 GGGACATGGGGTCCCAAGTGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGTCTTTG
 AGGGGGCTGTGGTGGCCGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCACG
 GAAGCCAGGGACAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCACG
 TGTCT**TAA**CAGTCTTCCCGGCTGCCAGCCCTGACTGTGGGGCCCCAAGTGGTCACTCCCC
 GTGTATGAAAAGGCCCTTACGCCCTGACTGCTTCTGACACTCCCTCCTTGGCCCTCCCTGTGG
 TGCCAATCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
 GGAATCTTACCAAGTGCCATCATCTTCACTCAGCAGCCCCAAGGGCTACATCTACAGC
 ACAGCTCCCTGACAAAGTGAGGGAGGGCAGCTGTCCCTGTGACAGCCAGGATAAAACATCC
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 TCAAGCGCTCTCAAGCACCCCGGCCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAATCTTCTGTCTGGCCTCCAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAAGGGACCTCACCCCTGGGGAAGTCCGAGGGGCTGGGAAGGGTTTCTGACG
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 TGTCCACAATATTCGTAGTCTCGACAGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
 CTGGCAGGAGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
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 AAAGA

FIGURE 28

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><subunit 1 of 1, 283 aa, 1 stop
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SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDAPDSRPEEALDSSRQLQADILAAATQNLKSP
TRAAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCCCTGGTGGGAGGAAGACTCTGGAGAGAGAGGGGGCTGGGCAGAG**ATG**
 AAGTTCAGGGGCCCTTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG
 CCCCTGCAGAGCGGAGAGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC
 TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG
 GCAGGTTCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG
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 GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCTTGGCCACAGTGGTGCTTGGGAACTTCTGG
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 GTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT
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 TCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT
 GCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC
 TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGG
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCCTCTGGGGA
 TCCAGCACCGGCTCCTCCTCCGCAACCACGGTGGGAGCGCGCGGAGGAAATGGACATAAAC
 CGGGTGTGAAAAGCCAGGGAATGAAGCCGCGGGAGCGGGGAATCTGGGATTCAGGGCTTCA
 GAGGACAGGGAGTTTCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTGGA
 GGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCT
 GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAAGGACCAGAGA
 AGCTCTCGCATCCCG**TGA**CTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACT
 CCCTCCTTAAACACCACCTCTCATCTAATCTCAGCCCTTGCCCTTGAATAAACCTTA
 GCTGCCCCACAA
 AA

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 30

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MKFQGFLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALQGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWQGQGGNGGPPNFGTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSSGSSSSGSSSSGSSSSGSSSSGSSSGSGSSGSGSSGSGSSW
GSSTGSSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
GGSGDNYRGQGSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCTCCGGTCTGTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCGGGGCGGTGCTACCG
 TGCCCTGGCTGGGCGAGTTCTCTCTCTTGTCTGACCATTTGTTTCCCTTGCTGGAATATTACGGGACATCTTCA
 CTCTCTCTGCTGCGGCTGCAGCGGAGCTTGGTGTGTGCGAGGAGGTGAGGGGGAAGATGCTGTTTCTGAAACAAGC
 TGCTGCTACTTGTCTCTCGGCTGGCTTTTCCAGATTCCCAAGCTCCCTGAGGACTTGTCTTCTCTGGAAAGAGG
 GTCCCTCATATGCGTTTGAAGTGGACACAGTAGCCCTCAGAGCATGGCTTGGACATGCGCTCTGGTGGACAGC
 AGCTGCTCTACAGCTGCTGCCCTACATCGGAGAGCTCCGGAAACTGCTCGCTCTGTTGGGTGTGAGGAGTAGTG
 GACCGAGTGGGGGCTTCATGAGGAAATACGCCCACTACCAACAGCTGGGAGGCCAGCTTCCAGAGCA
 GCCAGGGCTGCAGGCAAGCTCGCCAGGCCCTTTTCCACAACAGCGCCCTCTTGGCGGGACCGTAGAT
 TCGTGGCAGAAAGAAATGGATCAAACTGTGTCAAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCGCCAGG
 CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGAGAGGAGGGGGAGACCCAGCCAGCTGTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCAGGGGCCAGGCACTTGCCCTGGGGCGGAGTTCTGTCAAAGGAAGACCCCTG
 GGGCTGTGCGGGCGCTGCTCCAGAGGAGACCCCGGAGCGTCTGAGCAGTGACAGAAACATTGCTGTGGGGC
 TTGCAACACAGAAACCTGTGCTTGGCTGTACAGCAACATACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTGCACACTTCAGAGCCAGGCTCCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCCGAC
 GTGCTCTCCTTGGCGCTGGGGCCACGGGACCTGAAGAGGAGTCTCCCAAGAGCATCTGGAACAGCTCCTAGGC
 CAGCTGGGGCAGACGCTGCGGTGCCGCCAGTCTCTGTGCCACCTGCTGAGCAGCATCTGGCAAGGTCTCTGTG
 GAGTTAGCTTCCCTCTCTGTTGCAGATCAAAATCTTCTATCTAGGGCCCCGAGCAGTACAGGCTGGAGAGGG
 CAGGCTCGAGGGCTTCTGCACATGCTGCTTTCCTTGTGGAAGGAAGACTTTCAGGGCCGGTTCGCTGACAGTG
 CTGCTGAGGCCCAAGAAATGTGGGCTTCTGGCAGACACAGGCCAAGGAGTGGAGTCTGCTGCTATTCTTGCTA
 CGGGAGCTGTTGGAGAGGGCTGTATGGGACGGATGGAGATAGAGGCTGCTGGGACAGCTCCACCGAGGCCAG
 TGCCAGGAGTCTTGCATGAAAGATTAGCAACACTGTCTAATCTTTCTAGCCAGGCCCACTGCCAGAAACCC
 CAGCTTAAGACCTGTGAGTTGGTGCAGCCAAACCGGGCACTGTGCTGGCCCAAGAGTGGGGCTGAGAAGTGCC
 CTGCTTGGGCACTGCACCAACCTGGACCCCGCCTCAGAGGAGGCCAAGTGCCTAATGCAGACCTCCTAC
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAAGCTTCTGCTCTAAGGGTGTCACTGCTGGCATCCACACCGGGA
 ATCCTAGAGGAAGCAGAGTGTGGCTGATTGGGATTTAGGCAAAAAGCTCCAGAGATGCCAGTCTTGAGTAGAA
 GAGGTGGGTGTTTGTATCTCTTGGATCTAATGAAATGAGGTGTGGGGCTTGTACACAGAAATCAAGCTCT
 CATTTGCTATCCAGCACTCTTAAAACTTTGTAGTCTTGAATTCATGACAGAGGCAAGTGACTCCTGCTTAACT
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTCTTATACAGGAGCTGGAGTGCCTATCTCTT
 ATAAATGCTTAACACAGGCGGGTCTGGTGGCTCATGCTGTAAATCCAGCACTTTGAGAGGCTGAGGTGCGGG
 GACTGCTGAGGTCAGGAATCAAGACAGGCTGGCCAACTGGCAAAACCCATCTCTACTAAAAATAAAAAAA
 TTATTAGCTGGGCATGGTGGTGTGTGCTGTAATCCAGCACTACTCAGGAGGATGAGGAGGAGACCTGCTTGAAC
 CTGGAGGTGGAGGTTGAGTGCAGCGGAGTGCACCACTGCCTCCAGTCTGGGTAAACAGAGGAGACTTTTAG
 AAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCACTGAAACCTGACTTTCCTCCCTGTACCTTCAGCCCCTG
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCAATTAGAGCTTTTATGAATAAA
 CTGGTTTCTTTAAAAAAGGGCTTTTATTAATAATCTCCCAACAGATGGCTCCTGCAATCTGCCACAGCTC
 TGGGGCGTGTCTGTAGGGAAGGCCCTGTTTCCCTGAGGCGGGGCTGGGCTGTGCATGGGTCCGCGGAGCTC
 GCCGTGCTGGCGCCTGGCTGTGTCTAGCTGCTTCTGGCGGACACAGAGCTGCGGGGCTGCGGGGACCCGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCTGTCTTAAACGACACCTGAGGTGCTCTGAGATGCTG
 GGTCAACCTGAGTGGCAGGGGAGCAGCTGTGGCGGCTGCTCTTCTYTAGGCAAGTCTTGGGCAACTAAGCTC
 GGGCCCTCTTTTGCAGAAACGAGGATGGGTGGGTGTGGGGACTCATGGGGAATGGCTGAGGAGTACAGTGT
 GAAGAGGCGCGGTTTGTGGCTGAGCGGCTGGAGCGCTCTCTCCTGAGGCTCAGTTTCCCTTCCGCTCTA
 ATGAAGAACTGCCGTCTCGTGTCTCAGGGCTATTAGGACTTGCCTCAGGAAGTGGCTTGGACAGGCTCAT
 GTTATTTTCAACATGCTCTGCAGCTGTGGCTGGGCAAGTGTGGAATGGCCATGGCTCTGCTGCGGTGAC
 GTCCGGCTCGGAGTGGGCTGCCACAGAGGCGGGGCCAGAGCTGCGCTCGGGGTTGAGGAGGAGCGCCCGGAGGG
 CCTCACAGGAAGTTGGCTGCCGACCAACAGGAGGGCGGCTCCGCGCGGCCACACAGCTGCAGG
 GGCCTGAGCAAGTGAAGTGCCTGGGCTGCTGCGCAGAGTGGCCCTTGATGAGTGGCGCAGCGG
 TCGTCCGCAAGTGGAGCAGCGCCGCTCCACAGCACGAACAGCCGTGCGCT

FIGURE 32

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQFP
 SLRRTVEFVAERIGSNCKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
 IRREVKAASVRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGCTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCGAGCTTCCTTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTCTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAAATGAGGTCTTCCATTACGGGTCCCTGCGGGGGCGTA
 GCCGCCGACCTGTCAACCTCAAGAAATGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAAAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTACAGCAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACC GCGTCTGTGGCCCATTC
 AGTGTGTTCCGCGTCTGAGGAGGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT
 CATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC
 AGCGAGCGGGCCTGGTGTTCCTCCCAACATGGAAGCATATGCCGTCTCTCCGGCCGATGCGG
 CAATTTGACGACCTCTTCGGGGGTGAGACGGGCAGGACAGGAGAAAGTCTCATTCTGCGGTT
 GAGCAGCGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG
 GCATGTTCCCCCCTAACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGGCCGAGCAATGTGTACCTACATCCAGAATGAGCAGTCGCAAGGG
 CAACCACACCGCTTCATCACCGAGAAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA
 TCACCTTCTCCCAACCCCTCCTGGACC**TAG**GGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTT
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCCATGAGGCCCTGGTTGAGGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTTGGTGTG
 CCCCCTCAATTTCCAGCACCCAGAAAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAATTTGTGGGGTTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGA
 GGCTGGCATCCAGGCTCTGGCTCTGCCCTGAGACCTTGGAACAAACCTTCCCCCTCTCTGGG
 CACCCCTCTGCCCACACCAAGTTTCCAGTGCGGAGTCTGAGACCTTTTCCACCTCCCCACAA
 GTGCCCTCGGGTCTGTCTTCCCCGTCTGGACCTCCAGCCACTATCCCTTGCTGGAAGGCT
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCACCTCCTGGAAAACTTTAGGGTATTTTTC
 GCAAACTCTCTCAGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTCT
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCAGGCTCCTTTTCTGCCCT
 CTAGCAGGGAGGTTTTTCAACTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGCTCCGAGGGTCTCCCTCGACCTCTGTCTGCTGGGATGGCTGTCTGGGAGCTGT
 ATCACTGGGTCTGTCTCCCTGGCTCTGTATCAGGCACCTTTATTAAGCTTGGGCTCAGTGG
 GGTGTGTTTGTCTCTGCTCTTCTGAGCCCTGGAAGGAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGAGGGGACAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
 GGGCGGTGACTGGCCAGACTTGGTTTGTGAATTGTGACAGGAATAAACACACCTACGC
 TCCGGA

FIGURE 34

MSSNKEQRSVAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
 GNKTLPSRCHQCVIVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
 SSVFVRLRRPQEFVNRTPETVFIFWGPPSKMQKPGSLVRVIQRAGLVFPNMEAYAVSPGRM
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRLQRMPIYH
 YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPSTW

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

GTTTCATAGTGTGGCGTCTTCTAAAGGAAAACTAAATGAGGAACCTCAGCGCCAGGGAGCGCAGCGAGCTT
 GAGGGAAGCATCCCTAGCTGTTGGCCGAGAGGGCCGAGGCTGAAGCCGAGTGGCCCGAGGTCTCTGAGGGCGTGG
 GCGAAAGGTGAAGAGTTTTCGACAAAGCTTCTTGAACCCATGACCCATGAAGTCTTTGTGCATATTTATACCGT
 CTGAGGGTTCAGAGCTCGAAACTGAAGAAGTGGAGTGTGGCAGGGAGCGCAGTATCTCTTTGTGTGACCCCTGGC
 GGCCCTATGGGACCTTGGCTTCAGACCTTTGTGATACCACTAGCTGGCTGGGAGCATGACGGCGTGGAGAGGAATG
 AGGCGTGAGTGCACACTGGCTTGCTTCTCTAGCCACAGCAGGCTGTTTCTGTGACTTGAACCGAGTCTCCATCG
 GTCAACCTTCAGCGCTGGCTCCACCGCTCCAGAGCCCGGAGGCACTGTGATCTTGGGCTGGCTGGTGGAACTCCA
 AGGATGAATTAACCTTGGCGCTGAATGGAAGGAGCTGAATGGCTCGGATGATCTCTGGGTGTCCATCATCACC
 CACGGGACCTCGTCACTATGCCCTTAAACACCACACTGTGGGACGGTACCAATGTGTGGCCGGGATGCTCGCG
 GGGGCTGTGGCCAGCTGCCAGCACTGTGACATAGCAATCTCCAGGACTTCAAGTTAGATGTGCAGACAGTGT
 ATTGAAGTGGATGAGGGAACACAGCAGTCTTGTGCTGCCACTTGCTGAGAGCCACCCCAAAGCCAGGTCTCGGG
 TACAGCGTCAAAACAGAGTGGCTGGAGGCCCTCCAGAGGCTAACTACCTGATCATGCCCTCAGGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAACCT
 TCCGGCTTCAGCGCAGGCTACGTGTGGCCGCTCCACCGCTGAGGCTGCCGCATCATCTACCCCGCAGAGCC
 CAACCATCATCTCAGTCAACCAAGGCCAGAGTCTCATCTGGAGTGTGTGGCCAGTGGATCCCACCCACGGCTC
 CACTGGGCGAGGATGGGTCCAGTGTTCACCGGCTACAACAGAGCGGCTTTCTGTGAGCACTCTCTTCACTGAC
 ACCCGCAGGAGGAGCTCAGGCACTCACTGCTGCATGGCCGACATGGGCTGGGCAAGCCGGGAGCGGCTC
 ATCCCTTACATGTCCAGTGTGTGAACCCCTGAGGTCACTGAGGACTATCCAGCTGGTCACTCCCTGGGGC
 CAGAGTCCGAAGCTTACTGTGAGGTGGCTGGGAACCCCGCCCTCTGTCTGGCTGGAAGATGCTGTGCCCT
 CTATCTTCAGCGCAGCGCTCCGGCTCTCCCGCAGGGCCCTGGCGTGTCTCAGCATGGGGCTGAGGACGAAGGC
 GTCTACCAAGTGCATGGCCGAGAGAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTGGGACCTCCAGGCCAAGC
 ATAAACCCAGAGGCTATGGCAGGATGCTGAGTGGCTACTGGCACAACCTCTGTATCGGCTCCAAACTCGGCACG
 CCTGAGCAGTGTCTGAGGCGGCTCAGCCGCGCTCCCGAGCCCAAGCTCAGTGGGCGCTGCTTCCCGAAGTGT
 CCAGGAGAGAGGGGCGGCGGGCTCCCGCCGAGGCTCCATCATCTTCAGCTCGCCCGCAGCTCCAAGACAGAC
 TCATATGAATGGTGTGGCGGCTCGGCATGGGCACTGGCCGGGCGCCATCTCTACTATGTGGTGAACACG
 CGCAAGCAGTGCACAAATTCCTCTGACGATTGGACCATCTCTGGCATTCAGGCCAAGCAGACCGCTGACCCCT
 ACCAGACTTGACCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACCTGTGGGGAGGGCCAGACAGCC
 ATGGTCACTTCCGAAGTGGACGGCGGCCAAACCCGAGATCATGGCCAGCAAGAGCAGCAGATCCAGAGAGAC
 GACCTGGAGCCAGTCCCGAGGACGAGCCAGCCAGCCAGCCAGCCGCGCTCTCCCGCCAGAGCTCCGACAGG
 CCCCATCTTCCAGCGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCTGGGATGAGGTTCGCGCTCCAACT
 CAGTCTCTCGTGTGAGTACAGAGCTTAAGAAGTGTGGAGACTGGATTTGCGCACACAGGCACTCCCCCA
 TCGGGCTCTCGTGTGAGTACCGGCTTAGAAGAGGCACTCTACAAGTTTCACTCCGGCTCTGAACATG
 CTGGGGAGAGCGACCCAGCGCCCTCTCGGCCCTACGTGGTGTGGGGCTACAGCGGTCCGCTGTACGAGAGG
 CCGTGGCAGGCTCTTATATCACTTTCACGGATCGGCTCAATGAGACCCATCATGCTCAAGTGGATGTACATC
 CCAGCAAGTAAACAAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGCAGTGACATGATGAT
 GACTACAAGATGATATGGTGAAGGGGACAAGTACTGGCATCTCATCAGCCACTGCAGCCAGAGACTCCCTAC
 GACATTAAGATGAGTCTCTCAATGAAGGAGGGGAGAGCGAGTTACAGCAACCTGATGATCTGTGAGACCCAAAGCT
 CGGAAGTCTTCTGGCCAGGCTGGTCACTGCCAACCCCACTCTGCCCCACACAGCCGCCCTTCTGAAACC
 ATAGAGCGGGCGTGGGCACTGGGCGCATGGTGGCTCGCTCCAGCGACTCGCCCTATGATGTGCGGGGTCTGT
 CTGGGCTCATCTGTTCTCATCACTCACTTCTATCCCTTCTGCTTGTGAGGCGCTCGGTTCAAGCAAAAACAT
 ACAACAGACTGGGTTTTCCTCGAAGTGGCTTCCACCTCTCGCCGTATACATATGGTGCCATGGGAGGACTC
 CAGGCGCAACAGGCAAGTGGAGAGCCCTTACCTCAGTGGCATCAAGGACGGGCTGTGCTAATGGGATCCACATG
 AATAGGGGCTCGCCCTCGGCTCGAGTGGGCTACCCGGGCAATGAAGCCCGAGCAGCTGCCAGGGCGAGCTTCAG
 CAGCAGTGAACACAGGCTGCTGAGGCGAGACCCATCTTGGCAATGATATGACCCCAAAGTCCACAGT
 ACAGGGGTCCAAAGCTGAGCCCGAGAGGCTCTTCTGAACAGCTGGCCAGCCTCAGTCACTCACAGGCT
 CTGCGGCCCATCAGACTGCTCCAAACCGAGGAGCAGCTGCTGTGTGGGCGCAGTCAAGGGTGGAGGAGCC
 CCGCAGACTCTCTCTGGAGCAGTGTGGACCTCATTTCACTCAGGCCCCATGCTGCTGGGCGCTTGTG
 CAGTGTGAAGAGGTGGACAGTCTGACTCTCTGCAAGTGAAGTGGAGGAGAGTGTGTGCCAGCAACCCGTAGG
 GCCTACGTGAGGACGAGAACTGGATGCACTCTCCCGGGGCACTGGTGGGTGTGCTTTTGAACACCACTCT
 CTCACAATTTAGCAGAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAAAGAGAAAGAAA
 AGAGACAGAGAAATTTGTTATTTTCTTATTAAGCATTATTTATATTATGCACTTGTAAATAAATGTA
 TCTTATTTTATATTTCTGGAAGACATAAGGAGTCTTACCCGTTGAGGTGGAGAGGGAATTAAGAGAGTGGCA
 CACTAAGGAGTCAACCGAAGACACGCAAGGCTGGCGGGGACAGACTCTTAACCTGGGGCTCTGCAATG
 GCAAGCGAGGCTGCAAGGAGCCACAGATAAGCTGGCAAGGGAAGGATCCAGGCACTGGTTTCATCAGGCA
 TAGGGGAACAGCAAGGGGACCGGTATCAGACCTGGAGACACCAACAGCAGTCTGGTGTGCTCGGTGCTAGGGGA
 ACATTTCTCTAAGATGCCATGAGACAGACCAAGATGTGTACAGCACTGAGCAATAAAAAACCCTTCAGAAAT
 CAATATCCCTGGACACATATCTCTGTAAAAACAACACTGTACTCTAAATAAATGTTTATGCTCTCCCTGTAAAT

FIGURE 36

MLRGTMTAWRGMRPEVTLACLILLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPP
 RMNVWTWRLNGKELNGSDDALGVLIHTHTLVITALNHNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQDEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIYYPPEAQTIIIVTKQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFPEPPEVTMELSQLVLPWGQSAKLTCVVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLMSGPEDEGVYQCAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQFALPRPPTSVGPASPKCPGEGKGQGAPEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLLTLRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTRRRPKPEIMASKEQQIQRDDPGASQPSSSQPDHGRILSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFPIQSFVVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRPYVVSgySGRVYERFVAGPYITFTDAVNETT IMLKWMYIPASNNNT
 PIHGFYIYYRPTSDSDNDSDYKKDMVEGDKYWHSISHLQPETSYDIKMQCFNEGGESEFSNMV
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTMAMVARSSDLPYLIVGVVLGSIVL
 IIIVTFIPFCLWRAWSKQKHTTDLGFPFSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPSSAAVGYPGMKPQQHCFGELQQQSDTSSLLRQTHLNGYDQSHQITRGPK
 SSPDEGSFLYTLPDSTHQLLQPHHDCCQRQEQAAGVQSGVRRAPDSFVLEAVWDPFFHSG
 PPCCLGLVPVEEVDSPDSCQVSGGDWCPQHFPVGAYVQGEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCTGTCATGATCCGGACCCATTGTGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCACGGGCCGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGGGAGACCACGCCGGGCCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
 AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG
 CACCCCAAAACCTTGGACCTTGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCCACTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACCCATGGGCAGAGATTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTGAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTGTCTTATGCATCGGACACCTTGATAAGAAGGGTCTTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAAGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAAATTATGACGGGACT
 GGCCTGTTCCCTCAGGGCTGGAGGATGTGTCCACATACCCAGTCCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGACTTCAAGGTGTCTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGAAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCCTGGAGGTCTCAAATGCCT
 CCCCATACCTTGTTCAGGCCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCAGTGGCTC
 TGC**TGA**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCTCTCCT
 AGTTCACTCACAAAGCATATGCTGAGAATAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRLRLLLLLLLLLLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNLDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIFTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGTGGTGCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGTCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCTTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAG**ATGGGCTGG
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTCCTCCTT
 CTCCCTAAGTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTCGAGGCGGCCCTCAGGAGTGGATGCGATCTGTCTCTCTGGCTCCACTCTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAGCTGGGTCTTCA
 GGAAGTCAAGTGTCTGGGAGGAAAGCATGGCCAGCATTAGCATGTGTTCTCTTCTGCAGTG
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 AGCTGGTGTTCGCTGTCCCTGTGCATTCTCGCACTGGGGCATGGAGTGCCCATGCATCT
 CTGCTGCCGGTCCCTTCACCTGCATTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCTGTACTTTGGGTTGCCTCTTGTCCCTGAAGTTCGTTGTACCAAGTGCATGGA
 GAGAAAATTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATG
 TTTTATTTCTCTCA

FIGURE 40

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPFGHDVEAYCLLCECRYEERSTTTIKVVIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

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Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTTCGGCTAATTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCGCGACCCAAGTGAGGGGGCCCCGTGTTGGGGTCCCTCCC
 TCCCTTTGCAATTCACACCCCTCCGGGCTTTGCGTCTTCTCTGGGACCCCTCGCCGGGAGATGCGCCGGCTGTATG
 CGGAGCAAGAGTCTGCTCTGTGCTCCCTGCTCTACTGCGCGGTGCTGTATGTTGGAGAGCTCACAGATCGGCAGT
 TCGCGGGCCAAACTCACTCCATCAAGTCTCTCTGGCGGGGAGACGCTTGGTCAGCGCGCCAACTCGATCTGCG
 GGCATGTACCAAGGACTGGCACTTCGCGGGCAGTAAGAAGGCAAAAACCTGGGGCAGGCTACCCCTTGTAGCAT
 GATAGGAGTGTGAAGTTGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCTGCATGGTGTGTCGGAGA
 AAAAAGAGAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCGCTGCAATAATGGCATCTGTATCCCACTT
 ACTGAAAGCATCTTAACCCCTCACATCCGCTCTGGATGTTACTCGGCACAGAGATCGAAACCCGCTCATTTAC
 TCAAAACCATGACTTGGATGGCAGAAATCAGGAAGACACACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCAATTCGGACCAAAATCTGCAAA
 CCAGTGTCTCATCAGGGGAAGTCTGTACCAAAACACCGCAAGAAGGGTTCTCATGGGCTGAAATTTTCCAGCGT
 TGCAGTGTGCGAAGGGCTGTCTTGCAAAAGTATGAAAGATGCCACCTACTCCTCCAAAGCCGAGCTCCATGTG
 TGTGAGAAATTTGATCACCATTGAGGAACATCATCAATTCGACAGCTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAAAATAGGTTGAGATGCAGAAGAAATGGCTAAAAATAGAAACGTGATAAGAAATATAGATGATCAAA
 AAAGGGAGAAAGAAACATGAATGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCCTATTATG
 CAACTTGTCTATGTAAATAATGTACACATTTGTGAAAAATGCTATTATTAAGAGAACAAAGCACACAGTGGAAAT
 ACTGATGAGTAGCATGTGACTTCCAAAGATTAGGTTGTGCTGGAGGAGAGTTTCCCTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGAATAACTTGTTA
 TACATAGGTTCTAAAAATAAATGCTAAACAAGAAATGAAACATGGAGCATTGTAAATTTACAACAGAAAT
 TACCTTTGATTTGTAACACTACTTCTGCTGTTCAATCAAGAGCTTGGTAGATAAGAAAAAAATCAGTCAATAT
 TTCCAAATAATTGCAAAATAATGGCCAGTGTGTTAGGAAGGCTTTAGGAAGACAAATAAATAACAAACAAACAG
 CCACAAATCTTTTTTTCAAATTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTTCC
 TTCAGATTCTACGGAATGACAGTATATCTCTTTTATCTATGTGATTCTGCTGTAATGCATTATATTTTCCA
 AACTATACCATAAATTTGTACTAGTAAATACTTACACAGAGCAGAAATTTTCACAGATGGCAAAAAAATTTAAA
 GATGTCGAATATAGTGGGAAAAAGAGCTAACAGAGAGATCATTTGTTCTTAAGAGATTGGCCATAACCTATATTTT
 GATGCAATTAGATTGGTAAATCATGTATTCTATCATACTCTGTGTTAATAGAGACTTAAAGTACTGTACTG
 CACTGGAGTAGCAAGAAATTTGGGAAAACTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATGCTCTG
 AGGCACAAGTTGCGTGTCTATCTTTGAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
 CATATATTTACTATGCAAGTGAATTCAGTGTGAGTCTCTGTGTCGCTACTTCTCAAAATTTATTTTATATAG
 TGCTGAGATCCCAAAATAATCTCAATTTCAGGAGTTTCAACAAATGTACTCTGAGTAGACAGAGTAGGAGG
 TTTCAATGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCAATTTTCTCCCAAACTCTGCAAGCATCTG
 CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCGCCATTGCGGTTAAAAATAATAAGTAGATAACTGTAA
 AACTGCAATTTGCTAATCTATAGACCCACAGTTCTCAAAATCTTTGAACCACTTTACTACTTTTTTAACTT
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAGGTTATCTTATAGTCTGAGCTTAAACTTTGT
 TAGACCAAACTCACTTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAAATTAAGTTTCTCCAGTAG
 AGATTGAGTTTGAAGCTGTATATCTATTAATAAATTTCAACTTCCACATATATTTACTAAGATGATTAAAGCTTA
 CATTTTCTGCACAGGCTCGCAAAAACAAAATATAAACTAGTCCATCCAAGAACCAAGGTTTGTATAAACAGGT
 TGCTATAAGCTTGTGAATGAAATGGAACATTTCAATCAACATTTCTATATAACAAATTAATATATTTACAAT
 TTGGTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTAATTTTGAAGTAAATTTATTTACAGGAATG
 TTAATGAGATGATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAAATATTTTGCAGCTATTGAC
 TTTGTAAATTTAGGAAAAATGTATAATAAGATAAACTTATTAATTTTCTCTCTTAAAAACTGAAAAAAATAA
 AAAAAAATAAATAAATAA

FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
 FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNN
 GICIPVTESILTPHIPALDGTNRHNRHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
 SDCIEGFCCARHFWTICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
 SKARLHVCQKI

Signal peptide:

amino acids 1-25

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FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCTGACCTTGTAATCCACCTACCTTGGCCTCCCAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCACGTTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGCTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAATGGCAAACA
 TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTTCTCTCT
 CCTGGTTTGGAGTCCTTTCCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCACATGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG
 TCCACCAGCCACAGCCCCAACACATCAAACCTTGCTAAGCGGGCGGATACCCCCAGCTTCTAAG
 ATCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTTGATTGGAAGTCTTAAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCACTGACAGAACTCCACATATACAACCTCCGTCATTACCTCCTG
 CAGCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAACACACAGTTGGTCAATGGCTCATTTCGTTAAAGCAGCCCTTTTGCTTTTTGT
 TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATAAATCCAGTGCTTTGGGGGGCC
 AAGGCAGGCAGATTGCCCAAGCTCAGGACTTTGAGACCACCTTGGGCAACATGGTGAACCTC
 TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGCGCGCGCTGCCGTGAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
 PSTQQNSTSHPTTTTSDWLKPPTSQSSVLSHLDFKSQPEFSPVLSQLSQRQQHQSQAVTVPP
 PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPQPKHIKLAKRRIPPASK
 IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSQIPISLYSKSLSEPLNT
 SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
 GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKT PVGQWLIR

Signal peptide:

amino acids 1-24

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FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT
 TTGGA¹AAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 AC²GCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCACCTGGGACCGGCAGCCGCCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA
 CGGGCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCTGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGGCGCCCAGGCCAGC
 ACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTATCGTCCCCGAGAGCCGAGCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC
 TGTCTCCTGGCGCCCGCAGGCGCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGGAGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT
 GCAAATAGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCCCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCCACCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCCTGATGCCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAATGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCTCCAGGGCTGTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCAGGGACCTGTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTTGCCCATCCCTACCCTAGCCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCTT
 GGACTCTGCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACATAAAGTCCCCATCTGATTTTTAAAAA
 AAAAA

FIGURE 46

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDHRHVEEAQQVVHWDROPVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGFSLRIEPLLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPFPRGSPNGSSSHSGAPGDPPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLKGFRENCK

```

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGGCGTGGCGCAGCGCGACATGGCCGTTGTCTCAGAGGACGACTTT
 CAGCACAGTTCAAACCTCCACCTACGGAAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAAGCTGCTGGACCGCCGCCCTGGCCCTGCAGAGGCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTTCAGCCTGGGCATTTGGCAGTCTACTGCCATGGAACCTTCTTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCAGCCACCGGGA
 GGACCCCTGAGGGCTCAGACATCCTGAACCTACTTTGAGAGCTACCTTGCCGTTGCCCTCCACCG
 TGCCCTCCATGCTGTGCCCTGGTGGCCAACCTTCCTGCTGTCAACAGGGTTGCAGTCCACATC
 CGTGCTCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACCTGGTGAA
 GGTGGACACTTCCTCCTGGACCCGTGGTTTTTTTTGCGGTCAACATTGTCTGCATGGTGATCC
 TCAGCGGTGCCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCCTTTCCTATG
 AGGAACCTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
 CCACCATCTTCTCGTGCTGTCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCCTGTTCTTGCGGCCCATGTGTTTTCTGGTGAAAGAGGAGCTTCCCA
 GGACTCCCTCAGTGCCCTTCGGTGGCCTCCAGATTATTGATTTCCACACACCCCCCTCTCC
 GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACTACGCTCTTCTTCATCACC
 AGCCTCATCTACCCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
 GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACTTTGTGACCTAT
 GTGGCCGGCAGCTCACCGCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCCCTCCAGGG
 TTCGTGCTCCTCCGACCTGCCTCATCCCCCTCTTCTGTGCTCTGTAACACCAGCCCCGCT
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGTGCTG
 GGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGGCCCTAAGATTGTGCCCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTATGTGTGCTTGGGCTTAACACTGGG
 CTCAGCCTGCTCTACCCTCCTGGTGCACTCATCTAGAAGGGAGGACACAAGGACATTGGTG
 CTTCAGAGCCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCCATGGAGGAAGGCC
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
 GTGAGCCACCTCCATGCCATTCCGTGCAAGGCAGATATTCAGTCATATTAAACAGAACACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA
 ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTAC
 AAGCCAGTGCCAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCAGCT
 GACAGCGAGATGCAAGCAATGCTCAGCTCTCCTTACCTGAAGGGGTCTCCCTGGAATGGA
 AGTCCCTGGCATGGTCATGCTCCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCGGGTGAAACAACCTGCCACTAACAGACTGGAAAACCCAGAAGATGGGCCCTCCATGAAT
 GCTTCATTCCAGAGGGACAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTTCAAAAAAGAGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC
 TTTCACTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCTAAATAAATACTTGG
 GTATTCAAAAA

FIGURE 48

MAVVS EDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYYIFFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

FIGURE 49

CACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTCAACAAAGACTGGAGACACCA
TCTCCACCAGAGAGTCA**ATG**GGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC
TCAGCCTGGTGGCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
ATGCAGGATCCTGACTATGACGAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT
GAAGCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGCTGGTGGCCGCCAAGGTGC
TCAGCGATGCTGGACACAAGGTCAACATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCCAG
CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC
AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
AAGGTGCCCGAGAAGCTGGGTACGCCTTGGCTCCCCAGGAAAAGGGCCACTCGCCCAGAAG
CATCTACAGATGGCTCTCAACAGGCCCTCAAGAGCTCAAGGCACTGGGCTGCAGAAAGG
CATGAAGAAGTTTGAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC
CGGCGCGCGCTGCAGCTCTGGGAGGACGTGATGCCAGGATGGCTTCTTCTATCTCAGCTT
CGCCGAGGCCCTCGGGGCCACAGTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGTCCGGCTTGTGCTGTTGAAC
GCGCCCGTGGTGGCGATGACCCAGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGC
CGGTGAAGCGCATCACCTTCTCGCCGCCGCTGCCCGCCACATGCAGGAGGCGCTGCGGAGG
CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGACGGCCCTTCTGCGCGGAGGA
GCACATTGAAGGCGGCCACTCAAACACCGATCGCCGCTGCGCGATGATTTTCTACCCGCCG
CGCGCAGGGGCGCTGCTGCTGGCTCGTACACGTGGTGGACGCGGCGGCGAGCGTTGCGC
GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
TGTCGTGCGCCAGCTCTGGGACGGCACCGGCGCTCGTCAAGCGTTGGGCGGAGGACCAGCA
GCCAGGGTGGCTTTGTGGTACAGCCGCGCGCTCTGGCAAACCGAAAAGGATGACTGGACG
GTCCTTTATGGCCGATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA
GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCTGCAT
CGGACAGGCCACGCCCGAGGGGCGACGATCTGACATGGAGGGGCGAGGGCATGTGCATGGG
GTGGCCAGCAGCCCTCGCATGACCTGCACAAGGAAGAAGGACGACCCCTCCAGTCCAAGG
CCAGTTA**TC**TCTCAAAACACGACCCACACGAGGAACTCGCAT**TA**AGTATTTTCGAAAAA
AAAAA

FIGURE 50

MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGIALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSSEDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLPLRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRFPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVWRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIFYPAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGCGAGAAGCTGGGGACACTCTGGGCCGGCCTTCTGCCTGCAT
 GGAACGCTCTGAAGCCACCCTGCTCTCTGGAGGAACACAGGAGGGAAGAGACAGGGACTCGTGTGGCAGGAA
 GAACCTCAGAGCCGGGAAGCCCCCATTCACCTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGTCTGAATTTCTCT
 GCTGCTGTTTCAAAAGATGCTTTTATCTTTAACTTTTGTCTTTCCCACTCTCCGACCCCGGGCTTGATCTGCAT
 CTTGACATTTGGAGCTGCCATCTCTTTGTGGCTGATCACCAGAACCTCAACCCGTCTTACCTCTCTTGAACCTGAA
 CACTCAGTCTGTGGGAATTTGAGGGAGGAGCACGGAAGGGGGTTTCCAGAAGAACATGACCTTAAACAGTTGCTG
 CTTCTCAGATGCCAAGACTGTATGAGGTTTCCAAAGAGGACTCGCTGTCTGACAATGGGCCCTGCTTGGG
 ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGGTGCTGATAGAGCAGAGTACCTGGGTTCT
 CTGTCTCTTGCATAAAGGTTATAAATCATCACACAGACCACTTTGTGGCATCTTTGCTCAGAAATAGGCCAGAGTG
 GATCATCTCCGAATTTGGCTTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAAGAGC
 CATCGTACATATTTGTCAACAGGCTGATATGCCATGGTGATCTGTGACACACCCCAAGGCAATTTGGTGCTGAT
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCTGAAGGTGATCATCTTATGGACCCCTTTGATGATGACCTGAA
 GCAAGAGGGGAGAGAGTGGAAATGAGATCTTATCCCTATATGATGCTGAGAACCCTAGGCAAGAGCACTTCAAG
 AAAACCTGTGCCTCCTAGCCACAGAGACCTGAGGCTCATCTGCTTCAACAGTGGGACCAAGGCTGACCCCAAGG
 AGCCATGATAACCCATCAAAATATTTGTTCAAAATGCTGCTGCTTCTCAAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTTGAAGGATTTGACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTGCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTTGTTTCCCAGGCTGCTCTGACTCCTTAAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCTTT
 GAAGAAGTTCTTGTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAAGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTTGCAAAAGATCCAGGACAGCCTGGGCGGAAGGTTCTGTTAATTTGCTCATGGAGC
 TGCCCCATGTCCACTTCAGTCATGACATTTCTCCGGGACGCAATGGGATGTGAGTGTATGAAGCTTATGGTCA
 AACCAATGTCAGAGTGGCTGATCATTTACATTACCTGGGACTGGACATCAGGTCAAGTTGGGGTGGCCCTGGC
 TTGCAATTAAGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTTACAGTGAATTAAGAGGAGGTTGTCAT
 CAAGGTCACACAGCTGTTCAAGAGTACCTGAAGGACCTCTGAGAAGACACAGGAAGCCCTGGACAGTGAATGGCTG
 GCTTTCACACAGGACATTTGGTGGCTGGCTCCGAAATGGAACTCTGGAAGATCTGACCCGTAAAAAGACATTTT
 CAAGCTGCCCAAGGACATACATGTCACACAGAGAAGATAGAAAATATCTTCAACAGGAGTCAACAGTGTGTACA
 AATTTTTGTACACCGGGAGAGCTTACGGTCATCCTTAGTAGAGTGGTGGTCTCCACACAGAGTGTACTTCCCTC
 ATTTGACAGCCAGCTTGGGGTGAAGGCTCCTTTGAGGAACCTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT
 AGAAGACTTGCAGAAATTTGGGAAGAAAGTGGGCTTAAACCTTTTGAACAGGCTCAAAGCCATTTTCTTCATCC
 AGAGCCATTTTCAATGAAATGGGCTCTTGACACCAACATTTGAAGCAAGAGGAGAGCTTTCCAAATACTT
 TCGGACCCAAATGACAGCCTGTATGAGCACATCCAGGATAGAGATAAGGACTTAAGTACCTGCGCGGCCACTG
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 GATCCAGTGTATTGTTCTGTGCTCTTCTCATGATTTCCAACTTAACTACTATTAGTAACCAAGTCTCAAGGT
 CAAAGGGCCCTCTGTGCCCTCTTCTTTGTTTGTGATAAACATAAATTTGCCAACAGTCTCTATGCTTATTAC
 TCTTCTACTGTTCAAACCTAAGAGATTTTAAATTTCTGAAAACTGCTTACAATTCATGTTTCTAGCCACTCCAC
 AAACCACTAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGCTCCGATGCTCTT
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 TCTGACTTGGGAGTATTAATAATTTGGGCTCATGACATACTGTCCAAAGGAATGCTGTTCTAAAGCATTTATA
 CAGTAGGAGCTGGGAGTAAATCTGTTCCTACAGTTTGTCTGCTGAGCTGGAAGCTGTGGGGAAGGAGTTGACA
 GGTGGGCCCACTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAACCTCTGAACTGGGAACAAAGATCT
 ACAGGCAGCAAGATGCCACACACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCTTGGATT
 AGAGTTCTCGTCTACCTTACCCACAGATAACACATGTTGTTTCTACTGTAAATGAAAGTCTTTAAAAATAAAC
 TATTACAGATAAAAAA

FIGURE 52

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CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKFPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTPDDVAISYLP LAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKEQLQKGIIRHDSFWDKLI FAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTS GHVGVPLACNYVKLEDVADMNIFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDS DGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVQLQIFVHGESLRSSLVGVVVPD TDVLP SFAAKLG VKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPF SIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

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Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGGCCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG
 CCGGGGGCCCCTAAGCCATTCTTGAAGTCATGGGCTGGCCAGGACATTTGGTGACCCGCCAAT
 CCGGTATGGACGACTGGAAGCCCGAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTCGGAGATTCTGTCA
 GACAGGGGCGGTGCTTTTCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCTCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTCGACGTAGA
 GGTGTATTCAAGTCGACGAAGTATATGTGGCAGTGGATGCCACACGGTCTGGAGGATG
 AGGCCCCGGGAGCAGGGGCGGGGCATCCATGTCTATTGTCTCAACACGGCCCGGGCCACGTG
 ATGGCAAAACGTGTGTTTGACACGTACTACCTCATGAGGATGAGGCCATGGTGCTATTCTCT
 CAACATGGTAGCGCCCCGCGGAGTGCTCATCTGCACGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGCCCTTCTGGGACGAAAAGGAGGTCTGTCTTCTGGGGAGAAACATTG
 TAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCCCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGCTCGCCCGCGCGC
 TTCTGCAGCAAAAGTTAGGGCTATGGAAGTGTATGCAGCTGCAAGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAACAGGTCTCAATGTGGCTGTGGCTGTCTATTGAG
 GGAACCGACCCAAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTACAGCCAGGGGGTGCT
 CCTCAGATGATAACAGTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGACCT
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGTGTGGTT
 CTGGAAGAGGACTGGACATTTGCTGTGAGTTTTCAGTTTCTGAGCCAAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACAGGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCTGGGCTGGGTGGGTGCTC
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCTTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCGAACAACGCCGGGGCCGAGAGTGATCATCCCTGACG
 TTTCCCGATCCTACCACTTTGGCATCGTCGGCCCTCAACATGAATGGCTACTTTCAGCAGGCC
 TACTTCAAGAAGCACAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAGAAGCTTATGAAGTGAAGTTCAACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCTTTGAAGACTCTTCTTCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTGGAATGGAGAAAGATGATGACTTCAACACCTGGACCCAGCTTGCCAAGTGCCCTCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGCCCTGTGGAGATTGTTTCGGAAGAAGA
 ACCACTTCTGTGTGGTGGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCTCAGTC
 ACCCAATTTTCTGGAGCCACCCCCAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC
 ATGAGACCTCCTCCAGACCCCTGCGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCTTCATCTGTAGGATTTTGTAGATGCTGGTAGGGCTGGGGCTACCTTGTGTTTTAACA
 TGAGACTTAATTACTAACTCAAGGGGAGGGTTCCCTGCTCAACACCCCGTTCTGAGTT
 AAAAGTCTATTTATTTACTTCTTCTTGTGGAGAAGGCGAGGAGTACCTGGGAATCATTACG
 ATCCTTAGCAGCTCATCTTGCCTTTGAATACCCCTCACTTTCCAGGCTGGCTCAGAATCTA
 ACCTATTTATTGACTGTCTTGAAGGCTTGAAGACAGGCTGAGAGGCTGGATTTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCTTA
 GACACTGGACAGGCCCTCTCTCAGCCTTCTTGTCCAGATTTCAAAGCTGGATAAGTT
 GGTCAATTGATTAAGAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTVIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRNRRRFRFCCKVEGYGVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVVFIDGYEPEMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKKEAYEVEVHRLLSAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDLDVVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCATAAGAAGCTGAAAAGCCCACTCTCTTGGAAACCACCACAC
 CTGTTTAAAGAACCTTAAGCACCATTAAAGGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGGAGATGATGATTTCATCTCCATTAGCCTGCTGTCTCTGGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTCCTCTGGCTGTTAAATTTCTAGAGGAACGACTGAAGCTGGTGACTGTGTTGG
 GTGCTGGCCCTTCTCTGTGGAACTGCTCTGGCAATCATCTGCTGGAAGGATACATGCCCTTTATGAA
 GATATTTCTTGGGAAAAACCCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCATGAACATGAGCAGAGCCAGCACCACACAGACTGCATGCCATATATGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCGATTGGTAACCTCCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCACAAATCACCACCAGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTTCCTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGCCAGTTAAATG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTGGACTGTTTCCCTCTTGATGCATGCT
 GGCCTAGACGGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCTATGGCAGCACCAGTTATGTCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAAGCCCTTCAGAGGTGAACGCCAGGGAGTGG
 CCTGCTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA
 ATAGGCGCAGGCCACAAGCCGATGCCACGGGAGGGAGAGGCCCTCAGCCGCCCTGGAAGTGGCAGCCCT
 GGTTCCTGGGTGCTCTACCCCTCATCTCTGTCAGTAGGACACCAGCATTAATGTTCAAGGTCCAGC
 CTGGTGCAGGGCCCTTTGCCATCCAGTGAGAACAGCCGCGGACAGCTACTCACTTCCCTCAGCT
 TCTTGTCTCACCCTGCGCATCTCTACATGTATTCCTAGAGTCCAGAGGGGAGGTGAGGTTAAAAACCTG
 AGTAATGGAAAAGCTTTTAGAGTAGAAAACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAATATTTCTCTTAACCTATTTCTCAGGGAAGATG
 GAATTTAGTTTAAAGGAAAGAGGAGAACTTCATACTCACAAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAGCTATGCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT
 AACATGTTCCCACTGTAAGACTGGTGCTTTAGCATCTATGCCACATGCTGTTAGTGGAAGGTCATA
 GCACCACACTCATAGATCTTAAGGTTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAATGATAGC
 AAGACACATTGAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCTTTGGCAGCTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCAAAGAGGTGACTGGTATTTTGTAGCATTCCCTGTCAAGTTCCTCTTGACGAAT
 ACCTGTCTCCACATTCCTAGAGAGGAGCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCCTCAAGAA
 CAGTCAGATCACAAAGTGTCTTTGGAATTAAGGGATATTAATTTAAGTGATTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAAATGTATGGTTGCTCTTTTGTGTTTTT
 TTTTTTTTAAATTTCTCTTAGCAGTACGAATCCCTTAGGACCTAAATACCTTAGTGCAGCTTT
 GGGCAGACTGTGCTTCTCACATAACCACCTGTAGCAGATGGATCATAAATGAGAAGTGTTTGCCCTA
 TTGATTTAAAGCTTATTTGAATCATGTCTCTGTCTCTTCGTCTTTCTTTGCTTTTCTCTAACCTT
 TCCTCTAGCCTCTCCTCGCCCAATTTGCTGCTTACTGCTGGTGTAAATTTGTGTGGGATGAATT
 CTTATCAGGACACCACTTCTCGAACTGTAATAAGATGAATATCTTTATTTCTTTATCCCCTT
 CAAAGAAATACCTTTTGTGTCAAATGCCCTTTGTTAGCCCTTAAATACCACCTCTCATGTGTAA
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAGACACTAGGATA
 ATTTTTTTTTCATATTTGCCAAAATTTTGTAAACCTTGCTCTTGCATAAATAGTGTAATTTGTAT
 TATTAATTTATTTTACTTTCTTACCATTTCAAACACATTTACACTAAGGGGGAAACCAAGACTAGTT
 TCTTCAGGGCAGTGAGCTAGTAGTTTGTAAAAACGTTTCTATGAGCGCATAGCTAGCATGCCATG
 ATTTATTTCTCTCATGAATTTGTCTACTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTCTCT
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATCAGTTGTATGTAGTCAATGGCAACAATTGATACATA
 ATTTTACTACCAAGAGGATAGTATGGAAGTCCAAATGACTCTTGTATGGATGTTAACAGCT
 GACTGCTGTGAGACTTGAGGTTTCATCTAGTCCCTCAAACCTATATGTTGCCTAGATTCTCTCGGA
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCIYAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
 YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVEMLLVDQ
 IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
 APAAFGLVSFLMHAGLERNRIRKHLVFAALAPVMSMVTYLGLSKSSKEALSEVNATGVAML
 FSAGTFLYVATVHVLPFVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILLSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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FIGURE 57

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGCTCCGAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAA
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGTCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCAACAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTGAGTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTTGTATCCCCGACGGACAGGAGGAGCAGGAAGCT
 GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAAATTTACTTGATCAGCGTGAAAAGCGG
 AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAGAGATGACTA
 TAAATGTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

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FIGURE 58

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA
 VELKKNEFQGELEKQREQLDKIQSSHNFOLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
 KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
 SRDLSENNDQRQQLQALSEPQPRQLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR
 QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTFQVQAALSVSQ
 ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND
 RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

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FIGURE 59

GGAATGCAGAAAGCCTCAGTGTGTCTCTTCTGGCCCTGGGCTGCTTCTCTCTACGCTGGCATTGCCTCTTCA
 CCAGTGGCTTCTTGCTCACCCTGTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCCAGGCCCTGGGTGCC
 TGCCATGGGGAGCCAAAGGGAAACCTGGGGCTCTGCTGGATGGCTTCCGATTTTGC CGGGTTGTTGTTGGTCTGA
 TAGATGCTCTGCGATTTGACTTTCGCCCAGCCCCAGCATTACACAGTGCCTAGAGAGCCTCTGTCTCTCCCTACCTCT
 TCTCTGGGCAAACTAAGCTTCTTGCAGAGGATCCTGGAGATTACGCCCAACCATGCGCCGCTCTACCGATCTCAGG
 TTGAGCTCTCTACACCAACCATGTCAGCGCCTCAAGGCCCTCACCACTGGCTCAGCTGCCCTACCTTTATTTGATGCTG
 GTAGTAACTTCGCCAGCCACGCCATAGTGAAGACAATCTCATTAAAGCAGCTCACAGTGCAGGAAGCGGTGAG
 TCTTTCATGGGAGATGATACCTGGAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTTTCCCATCCTCTCA
 ATGCTCAGAGCTAGACACAGTGGACAATGGCATCCTGGAAACACTCTACCCCAACCTGGACAGCTGGTAATGGG
 ACGTGCTGATTGCTCACTTCTCTGGGTGTGGACCACTGTGGCCACAAAGCATGGCCCTCACCACCTGAAATGGCCA
 AGAAACTTAGCCAGATGGACCAAGGTGATCCAGGGACTTGTGGAGCGCTGGAGAATGACACACTGCTGGTAGTGG
 CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC
 TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACACAGAGGAGCCAGAGGTGATTTCTCAAGTTAGCCTTTGTGC
 CCACGCTGGCCCTGCTGCTGGGCTGCCCATCCCATTTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
 GGGGTGAGGACTCCAGCCCCACTTCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
 CCCGATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTTCATCAGCTCGCAGAACCTCT
 TCTCCAAGGCTCTGCTGACTACCAGTGGCTTCTCAGAGCCCCAAGGGGCTGAGGCGACACTGCCACTGTGA
 TTGCTGAGCTCAGCAGATTCTCTGGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC
 GCATCGGCGGGGTACTGCTGCTCTTCTGGCTGCTCTGCTTTATCTGCTCTGCTGGCATCTCAGTGGGCAATCCC
 CAGGCTTTCCATTTGCTCCCTCTACTCTGACACCTGTGGGCTGGGGCTGGTGGGGGCAATAGCGTATGCTGGAC
 TCTTGGGAACATTAGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGGAGCTCATCTCCCTCT
 TTTCTGTGGAAGCTCTGGCTGGCTGGGGGTCCAGAGGGCCCCCTGGCAACCTGTGTTCCCATCTGGGCGCGCTCC
 GTTACTCTGCTGTTTGCCTTGGCTGTGTTCTTCTCTGATAGTTTGTGTGAGTGGAGCCAGGCCACCCCTCT
 TCTCTTTGGGCTCATTCATCTGCTCTGCTGGTGTCTCAGCTTCACTGGGAGGGCCAGCTGCTTCCACTTAACTCTAC
 TCACAACTGCCCGCTTTGGCACTTCAGCACAACAAACCCCAAGCCCAATGGTGATATGCCCTGAGGCTTG
 GAATGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACTGTTGGCACT
 CCTCTCCCTGCTAGTCTCTCGCATCCATGGTGGTGGTGGTGGAGGCAAGAAATTAATGATGAGAGCTTGTGGT
 CGCGCTGCTGTTGGCCTGTAGCTCCGCTGGCTTGTGGCTTGC CGCTATGGTAATCTCAAGAGCCCCAGGCAC
 CCAATGCTCTTTGTGCGCTGGGAGCTGCCCTTAATGGCATTTGGGTACTGCTGCCATCTGGGCATTGGCGTGGGGG
 CAGATGAGGCTCCCCCGCTCTCGGGGTCTGGTCTCTGGGGCATCCATGTTGCTGCCCTGGGCTGTAGCAGGSC
 TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTCTGGTGAAGGCTGGGGCAGGCGCTCAA
 GGACAGGACTGCTCTCACTCCCTTCTCAGGCCCCCCCACTTCTCAAGCTCAGTTGGAATATGTGGTCCCTCAA
 TCTACCGACATGACAGGAGGATTCGGGGGCGGTTGAGAGGACAAATCTCAGGCTCCCCGTGACTGTGGTCTG
 CTTATCAGTTGGGGAGTGCTACTACAGCTGCTATGCTCACAGCCTCACCCCTTGGGCTTCCCCTCTCTGCTGT
 TGCATGCGGAGCGCATCAGCCTTGTGTTCCTGCTTCTGTTTCTGACAGGCTTCTTCTCTACATCTGCTTGTCTG
 CTGGGATACCGCTCACCAACCCCTGGTCTTTTACTGTGCTGAGGAGGAGGAGGAGCCACTGATGGAGATCGCGCTCCGG
 CACAGACCTTCTACTCCACAGGCCACAGCCTGCTTTCAGGCATCCATTGGCATGACAGCTTCTGTGGGATTC
 CAGAGGCTCATGGTCTGTTGCTTGGCTGCTTGTCTAGTGGAGGCCAACACTTCTGCTCCCACTCTCTCT
 TCCAGTAGGTTGCCACTGCTCTGCTCTGCGCTTTCTCTGTGTGAGAGTCAAGGGCTCGCGAAGAGACAGCAGCG
 CTTGGGGAATGAAGCTGATGCCAGAGTACAGCCGAGGAGGAAGAGGAGCCACTGATGGAGATCGCGCTCCGGG
 ATGCGCTCAGCAGCTCTATGACAGCACTGCTCAGCTGGGCTCAAGTACCTCTTTATCTCTTGGTATTTCAGATT
 CTGAGCTGTGCGTTGGGAGCTCCATCTCTCGAGGCACTCATGGTCTGGAAAGTGTGCGCTTAAGTTTCATAT
 TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCTGGGCAATAGCTTTGGTGATGAGAGTGGATGGTG
 CTGTGAGCTCTCTGGTTTCAGGAGCTATTCTTGGCCACGACAGCTAGCTAGTCTGTGATTACTGGCACTTGGCT
 ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTTGGATGATCTCAAGACAGGCTCAGGCATAC
 TCTTACTATCATGACGCCAGGGGCGCTGACATCTAGGACTCTATTATTTCTAATTCAGGACACAGTGGAGTA
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 CGGTGGTGACTTGCACCTATAATCCAGCACTTGGGGAGCAGAGGTGGGAGGATTTGCTTGGTCCAGAGATTCA
 AGACAGCTGTGGAACATAACAAGACCCGCTCTCTACTATTAAAAAAAGTGAATAAAATGATAATAT

FIGURE 60

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFIFYAGIALFTSGFLLTRLELTNHSSCQEPFPGPSLPWGSQKPGACW
MASRFSRVVLVLIDALRFDAQPPQHSHVPREPPVSLPFLGKLSLQRILEIQPHHARLYRSQ
VDPPTTMMQRLKALTGTSLPTFIDAGSNFASHAIVEDNLKQLTSAGRVRVFMGDDTWKDLF
PGAFSKAFFFPSPFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGFHPPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAAFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAEFLSGGEDSQPHSSALAQASALHLNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFASKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISSPGFFPCPLLLTPVWGLVGAI
YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPVPGVLLLLLFR
VFFSDSFVVAEARATPFLGSGFILLLVVQLHWEGQLLPKLLTMPRLGTSATNPNRHN
ALRLGIGILLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALV
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPFRLRVLVSGAS
RAVAGLAASGLALLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYR
EFRGLRLETKSQGPLTVAAYQLGSVYSAMVTALTLLAFPLLLHAERISLVFLLFLQS
LLHLAAGIPVTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFAIHWHAAFFVGFPE
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLLCSQGLRKRQPPGNEADARVRPEEE
LMEMRLRDAPQHFFYAALLQLGLKYLFIILGIILACALAASILRRHLMVWKVFAPKFIFE
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT
GTCTCTGGTGGTTTGCCATAAACCTGCAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
TCATCACAATTTGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
CCTGACAGCTCCAGAGAGTGGAAAGAGAAATCCAGAAGACCTTCTCTGTTCCATGCAACAAA
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAAACAGAACGTGGTCC
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
ACAGTGGAGTCCCTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAGAGCTAAATCATCTTCTGGTATGTTTTG
CCCATATCTATTACCGTGTCTTTTTCTGTGTGATGGGCTATTCCATCTACCGATATATCCA
CGTTGGCAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAATGAATTTGACAAA
GATTTCTTTGTGCTGCTGCTGAGAAAACTGTAATTAACCTTATCACCTCAATATCTCGGATGT
TCTAAATTTTCTCATCAGGATATGATGTTACTGGGAAAAAGCAGTGATGTATCCGAGCTTAA
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GGTATGCTTCGCATTTGATGGAATTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
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ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
AGGAGGTGTCACACAAGGAACATTATTGGAGTCGACGGCAGCGTTGGCAGTCTTGGGCCG
CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCTGGTGCAGTGGGATCCCC
AAACTGGCAGGCTGTGTATTCTTCTGCTGTFCAGCTTCGACCAGGATTGAGAGGGCTGCGAG
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTTCATGGAGGAATGGGGGT
TATATGTGCAGATGAAAAAC**TGA**TGCCAACACTTCCTTTTGCTTTTGTTTCTGTGCAAC
AAGTGAGTCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCAGTGTGTGATTG
GTTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCCTGGAGTCCAGGGGCTGGCCGGT
TGTTCTATCGACAGAAAGCAGTCAATAAATGTTTGCAGACTGGGTGCAGAAATTTATCAG
TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQ¹RVF²KEL³LL⁴TL⁵CS⁶ISS⁷Q⁸IG⁹PP¹⁰EV¹¹ALT¹²DE¹³KS¹⁴IS¹⁵V¹⁶LT¹⁷AP¹⁸E¹⁹K²⁰WK²¹R²²NP²³ED²⁴LP²⁵V²⁶SM²⁷Q²⁸
Q²⁹I³⁰YS³¹N³²L³³K³⁴YN³⁵V³⁶SV³⁷L³⁸NT³⁹KS⁴⁰N⁴¹RT⁴²WS⁴³QC⁴⁴VT⁴⁵N⁴⁶HT⁴⁷LV⁴⁸LT⁴⁹W⁵⁰LE⁵¹P⁵²NT⁵³LY⁵⁴CV⁵⁵H⁵⁶VE⁵⁷S⁵⁸F⁵⁹VP⁶⁰GP⁶¹PR⁶²RA⁶³Q⁶⁴P⁶⁵SE⁶⁶K⁶⁷Q⁶⁸
CA⁶⁹RTL⁷⁰K⁷¹D⁷²QS⁷³SE⁷⁴FK⁷⁵AK⁷⁶II⁷⁷FW⁷⁸Y⁷⁹VL⁸⁰P⁸¹IS⁸²IT⁸³V⁸⁴FL⁸⁵FS⁸⁶VM⁸⁷G⁸⁸YS⁸⁹I⁹⁰Y⁹¹RI⁹²H⁹³VG⁹⁴KE⁹⁵K⁹⁶HP⁹⁷AN⁹⁸L⁹⁹ILI¹⁰⁰YG¹⁰¹NE¹⁰²FD¹⁰³
KR¹⁰⁴FF¹⁰⁵VP¹⁰⁶AE¹⁰⁷K¹⁰⁸IV¹⁰⁹IN¹¹⁰FI¹¹¹TL¹¹²NI¹¹³SD¹¹⁴SK¹¹⁵IS¹¹⁶H¹¹⁷Q¹¹⁸DM¹¹⁹SL¹²⁰LG¹²¹K¹²²SS¹²³DV¹²⁴SSL¹²⁵ND¹²⁶P¹²⁷Q¹²⁸PS¹²⁹GN¹³⁰LR¹³¹PP¹³²Q¹³³EEEE¹³⁴V¹³⁵K¹³⁶H¹³⁷
LG¹³⁸Y¹³⁹ASH¹⁴⁰LM¹⁴¹E¹⁴²IF¹⁴³CD¹⁴⁴SE¹⁴⁵ENT¹⁴⁶EG¹⁴⁷TS¹⁴⁸L¹⁴⁹T¹⁵⁰Q¹⁵¹Q¹⁵²ES¹⁵³LS¹⁵⁴RT¹⁵⁵IP¹⁵⁶PD¹⁵⁷K¹⁵⁸TV¹⁵⁹IE¹⁶⁰Y¹⁶¹E¹⁶²Y¹⁶³D¹⁶⁴VRT¹⁶⁵TD¹⁶⁶IC¹⁶⁷AG¹⁶⁸PE¹⁶⁹EQ¹⁷⁰EL¹⁷¹SL¹⁷²
QE¹⁷³EV¹⁷⁴ST¹⁷⁵Q¹⁷⁶GT¹⁷⁷LL¹⁷⁸ES¹⁷⁹QA¹⁸⁰AL¹⁸¹AV¹⁸²LG¹⁸³P¹⁸⁴Q¹⁸⁵TL¹⁸⁶Q¹⁸⁷YS¹⁸⁸Y¹⁸⁹TP¹⁹⁰QL¹⁹¹Q¹⁹²DL¹⁹³D¹⁹⁴PL¹⁹⁵A¹⁹⁶QE¹⁹⁷HT¹⁹⁸D¹⁹⁹SE²⁰⁰EG²⁰¹P²⁰²EE²⁰³EP²⁰⁴ST²⁰⁵TL²⁰⁶VD²⁰⁷WD²⁰⁸
P²⁰⁹QT²¹⁰GR²¹¹LC²¹²IP²¹³SL²¹⁴SS²¹⁵FD²¹⁶Q²¹⁷D²¹⁸SE²¹⁹G²²⁰CE²²¹P²²²SE²²³GD²²⁴GL²²⁵GE²²⁶GL²²⁷SR²²⁸LY²²⁹EP²³⁰AP²³¹DR²³²PP²³³GE²³⁴NET²³⁵Y²³⁶LM²³⁷Q²³⁸FM²³⁹E²⁴⁰EW²⁴¹
GL²⁴²Y²⁴³V²⁴⁴Q²⁴⁵ME²⁴⁶N

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCGTGAAGCCCCCGCAGGCTCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCTGCTGCGAGCCCGTGGTGGTCTCGGCCGCCACTGCTTCAGCCACAGAGACCT
CCGCACTGBCCTGGTGGTGTCTGGGCGCCACGTCTGAGTACTGCGGAGCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCTTGTGCGGGCTGAACGGCTCTGCTGTCTTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAAGGGCCAGGCCCCCCACAGCGGGACACGGTGCCGGTGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCTCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGAGAGGGCCCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCTTCTCGGGCCTCTGGTTCGGGCGACCCCAAGACCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTCGCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC
CCGCCCCGGCCCCCTGAGCTGGGACCCACAGGCCCCCAAGGATGAAGCCGCCCTTGAGGCCAACCT
TCGCGGCGCAAAATGATGCGCCGCTCCAGGCCCTGGAATGTTCCGTGGCTGGGCCCCAGGG
AAGCTGATGTTTCAGGGTTGGGGTGGGACGGGACGGTGGGGCACACCAATTCACATGCA
AAGGGCAGAAGCAAAACCAGTAAATGTTAACTGACAAAAAAGAAAAAAGAAAAAAGAAA

ASGCTACCCAGGCGCGTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCTGACGCGTGA
CGCTGTCCCGGCCCCGGC**ATG**AGCGCTACCTGCTGCCGCTGTGCGCGCTGGGCACGGTAG
CAGGCGCGCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
ATCCTTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
GGAAC**T**GGCCAGAGAGGAGGCAACATCATCTTGGCCTGCCGAGACATGGAGAAGTGTGAGG
CGGCAGCAAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCCCGGCACCTGGAC
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCGAGCAAAGATCATTGAAGAGGAGGAGCGAGT
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
TCGAGATGCAGTTTGGCGTTAAACCACCTGGGTCACTTCTCTTGACAAACTTGCTGCTGGAC
AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
CCAGAGCAAGCTCGCCATCGTCTCTTCCACCAAGGAGCTGAGCCGCGGCTCGAAGGCTCT
GGGTGACATGTCAACGCCCTGCACCCCGGCTGGCCAGGACAGAGCTGGCGAGACACGCGG
CATCCATGGCTCCACCTTCTCAGACACCACATCGGGCCCATCTTCTGGCTGCTGCTCAAGA
GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
TCCGGAAGTACTTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA
GGGAGCAGCCCTCCCCAGAT**TAA**CCCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAG
GACTGGCGGCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC
CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
AGGGGCCATCTGATGCTTCCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGGCTC
TGTGCAC**T**TGCAGGCCACGTGAGGAGGCCAGCGGTGCTGTGCGGGAGGGTTCCAAGGTGC
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTACGAGTGAGATGCTCAGAATAACTG
CTGTCTCCCATGATGGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
GGTGGTTTGTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTATCCC
GAGTTCTAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
TGTCCCTGGGACTCCCACTTCCATCAATTCTCATGGTAGTCCAACCTGCAGACTCTCAAC
TTGCTCATTTT

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNLGHFLLTNLLLDKLKASAPSRILNLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSQVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPFIWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQLPR
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Signal peptide:

amino acids 1-17

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FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGTACTTTCTTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCCTGCTGCTGCATTTACTCTCATCAACGCCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCCTTTGAGGACCTTGAGGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGCCCTGGCCGAGGTGCTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTTCCATGGCTGGAGGAGGTGTCACTCTTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACCCAGTGGTAGC
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 TATGTACAGCCCTGGGTTCCAGCCCACTCTCTACAGATCCCTAGCCTCTACTGTTCCCTAT
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCTGTCAGTGACTCAGAGGCTCAGAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCCTCAA
 CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCAACCAAGC
 AGCCCCCTCTACAGAAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTCACTATGCCAACCTCAGCGTGGCTGTGGTTAGGA
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGTCTGTTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG
 ACAGGAATTCGCGAGCCCTGCAGCTCCAGCCCTGAAGACT**TGA**ACTGTTGGCAGAGAGAAGC
 TGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCACTTTGTCTGTGCCCTCGCAAATCAGAGGC
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 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTG
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 TTTTGGCACTTTGAACCTTGACCAAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCACTGCCTTCTGCTGCAGCCCAAG
 CAGGAGTGTGCCCCCTCCAGAAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTCTTTCTTTTGTATGATGTTTTTTAACACAGTCATTAATAA
 ATGTTTATAAATCAAAA

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLLKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQVRVTSIAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPLQTRDTYEGLCQTIGS
QPTLYQIPSLYCSYETNSNAYLLQLPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVAVSGHKQLQVEYRISKSAWLKNRVTDPKLVLTLNHRHIAATGLDVRPPYAEYLQVVNYGIG
GHYEPHGDHATSPSSPLYRMKSGNRVATFMIYLSSEVAGGAATFIYANLSVFPVRNAALFWW
NLHRSPEGSDSTLHAGCPVGVGDKVANKVHIYEGOEFRPCSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAGTTCCCTGCTCCATCTCAGGAGCCCCCTGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGTGGCTGAGGGACCGAGCCGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG
 CGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCCCT
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAGTGCCCTCC
 TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTGCATGTTTCATGGTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
 ACTTCCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
 AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATTGTGTGGCTACAAAACATTCGAC
 AAGGAGCGTTTTCAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCGGTGATCAT
 CTGGTTTCATGGACAACACACCATTATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATACCCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTGTGCTACCCCAATTAGGGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCTGTGTGTAGGTCCCACGGCCTTGCCCTC
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 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGC
 CTCCTCTCAGCCTCCAGGTGCCCTTGAGCCCCTCTTGCAAGGGCGGGCTGCTTCTTGAGCCTA
 GTTTTTTTTTTACGTGATTTTTGTAAACATTATTTTTTTGTACAGATAACAGGAGTTTCTGAC
 TAATCAAAGCTGCTGATTTTCCCGCATGTCTTATTCTTGCCCTTCCCCCAACAGTTTGTAA
 TCAACAATAAAACATGTTTGTGTTTTTAAAAA

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 0.100

FIGURE 70

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
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AII LILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGCTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAG**ATG**CGCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCACATGACGACTGAGGCCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA
 TTGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC
 AGGTTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAAGCTGTGTCCCGTG
 ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTTC
 CCTCAGCATTGACCCTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTTC
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCTTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA
 GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCTCTGTGG
 ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA
 GTGAAGCCCTCCGCCCTTTGTTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTATAC
 ACCAAAGGTGACCAACTTATATCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG
 AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGGAACCCAGCTCTCCTGTCTCCAG**TGA**AGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAAACACTTGCCTGTGAAAAA

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 400
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FIGURE 72

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><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSEAL
RPLFTLGIEASSEAQFYTKGDLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLT KDALVLT PASLWKFPSSPVSQ
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Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATG**GCAGCGGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTGGCAGCGTTCCCTCAGCCCTCTGCCCAAAGAAAGAAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAAATGAATGGAGACA
 AGTTC CGTCGCCTTGTGAAAGCCCCACCGAGAAATTA¹CTCGTTATCGTCATGTTC²ACTGCT
 CTCCA³ACTGCATAGACAGTGTGTCGTTTGAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AA⁴ACTCCTGGCGATAC⁵TCCAGTGCATTACCAACAGGATATTTTTGCCATGGTGGATTTTG
 ATGAAGGCTCTGATGATTTT⁶CAGATGCTAAACATGAATT⁷CAGCTCCA⁸ACTTTCATCAACTTT
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGTTTTT⁹CAGC
 TGAGCAGATTGCCCGTGGATCGCCGACAGA¹⁰ACTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCTTATGTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTTCGAAGAAGTAATATGGAATTTCTCTTAATAAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGC¹¹TTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGGCTGGTATTG
 GACTTGTTGTATTATTCTTCA¹²GTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGT**TAAAA**AGGTCCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAA¹³AATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGATTAC
 CTC¹⁴TTTTTTTCAAGTGATTTAAATAGTTAATCATTTAAACAAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAA¹⁵AATCTGAGGTATTGAA¹⁶AATAATTATCCTCTTAACCTTCTCTT
 CCCAGTGA¹⁷ACTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAATTTGAAAA
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 ACTTTACGCATCTTTCCTTTT²⁰GAGTAGAGAAATATGTGTGTCTGTGGTCTTCTGAAATG
 GAACACCATTCTTCAGAGCACACGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
 GCATATTTCCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTAGAAA
 GATTTCAGATTCA²¹TCCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAAATA
 TAGCTTAGTGCTAA²²AATCAGTGTAACCTATACATGGCCTAAAATGTTTCTACAAATTAGAGT
 TTGTCACCTATTCCATTTGTACCTAAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
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 GAGGTCAAGAGTTCGAGACCATCTGGCCAACATGGTGA²³AACCCCGTCTCTACTAAAAATAT
 AAAAATTAGTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC
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FIGURE 74

MAARWRFWCVSVTMVVALIVCDVPSASAQRKKEMVLSEKVSQLEWETNKRPFVIRMNGDKFR
 RLVKAPPRNYSVIVMTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
 SDVFQMLNMNSAPTTFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
 AGPLMLGLLLAIVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
 PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMGMVLLCEAATSDMDIGKRKIMCVAGIGLV
 VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

[illegible]

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
 <subunit 1 of 1, 536 aa, 1 stop
 <MW: 61450, pI: 9.17, NX(S/T): 7
 MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRLTFHFGSQVVKLPFFINF
 MKTRGTSFLNAYTNSPICCPRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
 KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDWQNTDKAVNW
 LRKEAINYTEPFVIYLGNLPHYPSPSSGENFGSSTFHTSLYWLEKVSFDAIKIPKWSPLS
 EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
 SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQSVNVVSLVDIYPTMLDIAGIPL
 PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
 ILPQLFDLSSDPDELTVNAVVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
 QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
 498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCCTTCTGGGGCTTTTGGGCACACT
 GGTGCCATGCTGCTCCCCAGCTGGAAAAAAGTCTTATGTCCGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCAGAGGCATACCCAG
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCAGGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTCACTCCTGTTGCTTGGGAATCTTCATGGGATCCTACGGGA
 CTTCTACTCACCAGTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCCTTTTACTTGG
 GCATTATTTCTTCCCTGTCTCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
 ATGTG**TGA**AAGAACCGGGGCCAGAGCTGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
 CCCTGCCCTAAGTCCCCAACCTCAACTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
 ACTGACCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATGTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTC
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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FIGURE 78

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYYLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
```

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**CATG**GTGCCCAGAATCTTCGCTCCTGC
 TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
 AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
 TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
 CTTCTGGCCCTGCTTTGAGCTCTGTCTTGTATTCTTTGGCCTCACAAACGATTTTGTG
 TGAAGCTGAAGGTTTCAAGGTGTGAATCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
 GAAAGCAGAAGACGTTTTCCCT**TCAG**GAAGACATAGAAAGAAATCAACTTTCACCTAAGGCATC
 TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
 ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
 AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 80

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPNLCQPAAPRCGDKIYNPLEQCCYNDAIVSLSE
 TRQCGPPCTFWPCFELCCLDSFGLTNDFFVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

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FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
 TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
 GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT
 GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGAAACTGCACCTTCAGA
 GTCTGCTTTGAGCAGTGTGCCCCTGACCTTCATGGTGAAGCTGATAAACCAGAACTGCCA
 CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTAATGGAACATCAGGGGAA
 CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
 TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT
 CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
 AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCCTCCTGAT
 GACCCCTATGGCCAACATCAACCCGGCACCACCCAAGGCTGGCTGGGGAACCCCTTCACCCCT
 TCTGTGAGATTTTCCATCATCTCAAGTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
 TAAATTTATGTACTTTATAAATGAAA

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FIGURE 83

GGGGGCGGGTGCCTGGAGCAGGCGCTGGGGCGCCCGCAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCGCGCCGGCCGCTCCCGCCGCTCCCGGCACACAGAAGTTCTCTCT
 GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG
 CACGCCGTATTCCCTGTATGTCTGTCCGAGGGGCAGAACGTCAACCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCAGCATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCCAAAGATGCACCATCCAAGTGTGTGGTGT
 ACCCATCTCTCTCCAGGATAGTAAACATCAGGCTGCAGCCCTGGCTACGGGTGCTCTGC
 ATCGTAGGAATCTCTGCCCTCCCTCATCTGCTCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCACGCGGAGCCTTCTGAGTCTGGGCGCATCTGCTTTCGGAGCCACGAC
 CCCCCTGTCTCTCCAGGCCCGGAGAGCTCTTCTTCCATCCCTGGACCTGTCCCTGACT
 CTCCAAACCTTTGAGGTCATCTAGCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
 GGCAGGTGCATTTAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCGAAGGATTTTGGGCTGCTGAG
 ATTCTCCCTCAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCCGTGGCCGCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC
 AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC
 ACCTTCCCCAGCTGCCTCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATCCAGTCCCAGAGCTTGGTGGTCCCAGAACGGGAAGTAC
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCACTGGAGATGGTGTGAGGGAGGTGGTGGGGCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCCTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLTLDGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCTCTGCCCTCC
 TTTCTTGCCACCGCTGCTTCTTGCCCTTCTCCGACCCGCTCTAGACAGACACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTCTCCTTTTCGTCTCCCTTCCTCCCGA
 CTCGCTCCCCGACAGCGGCTGACCTTGGGGAAAGGATGGTTCCCAGGTGAGGTCCTC
 TCCTCCTTGCTGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCC
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCTACT
 TGGAGCCACAAGGCCTGATGTA CTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTACCGCCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAGTCCTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCA GTGCCCATGAGCTGTTCCCTCC
 CGCTGCCCAACCACTGTGTCTCTG CAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGTCTGCCAAGCCT
 GCAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTTCATCCCTCGCACTTCAGACCCAAGGAGCAG
 GCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCCACGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGT
 ACCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCACAGGACAAA
 GCAGACCTTGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAGGCACCGGGCCGGTCTCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCCTCGCTTTGCCCTGGAACACAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC
 GAAGGTCACCTGGAACGTCTTCTAGCCAGACCCCTGGAGCTGAAGGTCACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSLLGLALLWFPLDSHARAPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCQPVTPEQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGCAACAGCTTGC GGCTGCGGGGAGCTCCC
 GTGGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTCTTGC GGAATGCTGATCTCAGT
 CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGAG
 AGCGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGAGGAG
 GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
 CGTGGCCTGGAGGAAGAACTGGATGGTTGGCGCGAAGGCGGCGCCAGCGGGAGGTACCCGT
GAGACCGGACTTGCCCTCCGTGGGCGCGCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCC
 TTTCTCCTTCGTGGGCCCAGCGGAGAGTCCGGAACCGAGATACCATGCCAGGACTCTCCGGGG
 TCCTGTGAGCTGCCGTCGGGTGAGCACGTTTCCCCAAACCTGGACTGACTGCTTTAAGGT
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 TCATGTTCTCCAA
 AAAAAAAAAA

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FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPIQDPRSREEAARTQQLLLA
 TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

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[illegible]

FIGURE 90

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLLILFLLSWGPLQGQHHHLVEYMERRLAALERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVVPFPWVGTLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAGEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTQ
QWDTPCPRENAEAAAFVICGLTYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

```

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
 CCGTACCTCTCCTGTATCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCCTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTCTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGAAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCACAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGTACTCTGTCTAGTCTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG
 GAAAGGTTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCTGTTCATGA
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAAAAATCCAGGCGGAAGTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACTGTAACCCATA
 GAAAAGCTCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCTCAGACTGAATGGAGAACATTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAACCTCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTCTTGGCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGG
 GTGAAATG**TAGG**ATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGTCTCTCTCCCA
 GATCCAAAGTCCCAGCAGAGCCGCCAAGGTGGCTTCCAGATGAAGGGGGAGTGGCCTGCC
 ACATGGGAGTCAGGTGTATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACC
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGATCCTAATGGTTTGTTTCATTATATACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFCFLSPKTNAEAMEVRFFRGQFSS
 VVHLYRDGKDQPFMQMPQYQGRITKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
 AIWELQVSAALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGDLSTDSRTNRDMH
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
 FGIVGLKIFFSKFQWKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
 HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL
 PDHGYWVLRNLNGEHLFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSILIYTLT
 RFEGLLRPYIEYPSYNEQNGTPVICPVTQESEKEASWQRASAIPESTNSSESSQATTPFLP
 RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGGCGGTTGCGGAGGCTTCCTTGGTTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
CATGAGGAGCCTGCCGAGCCTGGGCGGCCCTCGCCCTGTGTGCTCGCGCGCCGCCGCCGCCG
 CCGTGCCTCAGCGCCTCGCGGGGAATGTACCCGTGGCGGCGGGGCCGCCGGGGCAGGTG
 GACGCGTCGCCGGGCCCGGGTTCGGGGGCGAGCCAGCCACCCCTTCCTTAGGGCGACGGC
 TCCCACGGCCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCGATCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC
 ACCACCTTTACGGCGCCGCTCGGCCCTCGCCGACCACCCCTCGGCGGCGGAACGCATCTT
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCGGACCACCCCTTCGACGACCACTGGCCCCG
 CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCG
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCTCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCTCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGCGAGTGTGAGTGTGGCCAGGTTATCAGGGGCTTCACTGTGAAACC
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAAGTGAAGTTTATT
 TTATTTTAGCAAGGGAAGAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTACAAAAATTTTATATACCTTTTATCTCTTACTTTATATGT
 TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTCTCTCAAAGCACTAG
 AGTCGCCAATTTTCTCTGGGATAATTTCTGTAATTTTCATGGGAAAAAATTATTGAAGAT
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
 ATCAAAATTCACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCCTAATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACAGTACATTTTGGAGCCAAAAG
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTGCGCTTGACTGCACTGAAAGTAATTTATCTTTGACCT
 TATGTGAGGCACCTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTTACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTTGGCAAGTAATTTCTTTCACTGAGCTTGTTCCTCTCAAG
 GTTGTGTGGAAGATTAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTTGTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTAAAG
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTATACGTTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCACGCTGTAATCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGTCTCTACTAAA
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCAGCTACTCGGGAGGCT
 GAGGCAGGAGAATCGGTGAACCCGGGAGGTGGAGGTTGAGTGAGCTGAGATCGGCCACT
 GCACCTCCAGCCTGGTGAGAGAGGAGACTCTGCTCTAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLGLGLALLCCAAAAA AVASAASAGNV TGGGGAAGQVDASPGPGLRGEP SHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPRTPTPDL PSSSSNSSVLPTPPATEAPS
SPPEYVCNC SVVGS LNVRNCNQT TGQCECRPGYQGLHCETCKEGFYLN YTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGC GGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
 TCTCGGTGCCAGGGCCAGGCCGTGTGGTTGGGAAGACTGGACCTGAGCAGCTTCTTGGG
 CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
 GAACGTGCTGGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
 AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAACTCCGGATGG
 GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
 CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
 ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC
 CTGGGCTTCCTGTACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
 CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
 GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCCAGCACCAGCTCAGAATAAAGCGATT
 CACAGCA

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FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
 LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL
 EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

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FIGURE 97

AACAGACGTTCCCTCGGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGACGGAAGGCCTGTGTGCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGCTGGATTACCTTGGCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA
 CCAGSATGCTCCAGTGGCCACAAACACCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGAGATACTTCTTTCTGATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
 GCACCCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGTCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCCAGCGTGACCAAGAACAGACCGTCCATCTCAACGTGTCTTAC
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCACTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCCTGGGTGCACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAACGCTGTCAGGGGTTACGCT
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGAT**CGA**AAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPPVHHGYWF
 REGANTDQDAPVATNNPARAVWEETRDRFHLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
 SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVFWACEQGTTPMISWIGTSVS
 PLDPSTTRSSVLTLLIPQPDHGTSLTCQVTFPGASVTNKTIVHLNVSYPPQNLMTVFQGDG
 TVSTVLGNSSSLSLPEGQSLRLVCDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
 HLRDAAEFTCRAQNPLGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
 CRKKSARPAAGVGTGIEDANAVRGASQGPLTEFWAEDSPPDQPPASARSSVGEGELQYA
 SLFQMVKFPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCCGCAGCACAGAGCTCTGGAG**ATGA**AGACCCTGTTCTCTG
 GGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCCTGGAGGAGGAGGATATCACAGG
 GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCAGGA
 AGGTGTCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
 ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
 ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT
 ACATCTTTTACTGCAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
 AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
 ACTCTCGGAGGAGGACATTTTCACGCCCTGCAGACGGGAAGCTGCGTTCCTCGAACAC**TAGG**
 CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
 GGACCTACCCTCCAGCCATGACCCCTTCCTGCTCCACCCACCTGACTCCAAATAAAGTCCT
 TTTCCTCCCAA

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</usr/seqdb2/ssr/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTFLFLGVTGLAAALSFTLEEDITGTWYKVMVVDKDFPEDRRPRKVSVPKVLTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPKQKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSRDNTREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA
 TCCTGCTTGTCTGGCAACAGGGCTTGAGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG
 TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
 GCGGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
 TAGTTCACTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
 AGCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
 GAAGTGTGAGAACGCCTACCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCCCTCTGGTCTGTAACCACTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTTTGTTGTTCTGTCTACTCTGTTAAT
 AAGAAACCCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
 GAAATATTGTGACTCTGGGAATGACAACACCTGTTTGTCTCTGTGTATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCSLISGWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTM
VCASVQEGGKDCSQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

```

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCGTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTACAGATTCATTGTTT
 TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAGAGAGCACCAGAGAA
 GTGAAAATAGAAGTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
 ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATCTACTGCAGCCGGA
 CACAAAATGAAGGCCACCCCAAATGGTTTGTTCTTGGTGTTGGGCAAGTCATAAAGGCCTA
 GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
 TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCACCGGATGCTACATTGATTTTTG
 AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
 ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTGA
 AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTTAAGA
 AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
 GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
 AAACAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCTATGAGAAGATATTTTGA
 TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTCGAACTTAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLVGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDDHGDGFISPKEYNVYQHDEL

```

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

CAGAAATG CAGGGACCAT TGTCTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAAACAAAAC TTCTGTGCTAAGTGCCCCCAAATGCTTCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAAACATTACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTGAGAGTTTGAGACCAGCCTGGCCAACATAGTGAAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAAC TCAAGGAGGAGAGTTGCACTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGCTCTAAAAAGAAAAAGA
TAGTTTCTGTTTCATTTGCGGACTGCCCTCTCAGTGTTCCTGGGATCCCCCCTCCCAATAA
AGTACTTATATCTC

FIGURE 106

MQGP~~LL~~LPGLCFLLSLFGAVTQKT~~KT~~SCAKCPPNASC~~VNN~~THCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL

Signal peptide:

amino acids 1-18

106/249
MQGP~~LL~~LPGLCFLLSLFGAVTQKT~~KT~~SCAKCPPNASC~~VNN~~THCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL
Signal peptide:
amino acids 1-18

FIGURE 107

CAAGCAGGTCATCCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGGCAGAGGTGGGGGGCAC
 AGGAAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGCTTATTGACCACAGGTGGGTCTTACAGCGGCTCACTGCA
 GCGGCAGCAGGTAAGTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCAGGTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCCTGCCCCCTGCCCAATGACTGTGCAACCGCTGGCACCAGTGCCACGTCTCAGGCTGGGGC
 ATCACCAACCACCCACGGAACCCATTCCCAGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCGGGCAGGATGCCAGGGTGATTCTGGGGGCCCTTGGTGTGTGGGGGA
 GTCCTTCAAGGTCTGGTGCTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGATGATCATGAGGAACAAC**TGAC**
 CTGTTTCCCTCCACCTCCACCCCCACCCCTTAACTTGGGTACCCCTCTGGCCCTCAGAGCACC
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTGTGTGGCCTGGGAACCTCTTGAACTT
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV
 QPLPLPNDCATAGTECHVSGWGITNHPRNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC
 AGGVPGQDACQGDGGGPLVCGGVLQGLVSWGSGVPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

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FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGAAGGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTCACTGACACTATATCCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTGTTTGGTCATTGAGGGTTTGTGTTGTGTTT
 TCATCAATGTCTTTGTAAAGCAGAAATATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
 TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTTGGAGGAACACGACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTCTTTCGGGTTTCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTCACCC
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAGGAGCTTGGCATTGGGAGGCCCTTCAAGAAGG
 TACCAGAAGGAACCTCCAGTCTCTGCTCTCTGCCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGACAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
 GGGTTTGGGGGGAAGGTGAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTTGCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 111A

CGCGCTCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCCTCTCCA
 GAGAGCGGGCCCTGCACACCA**ATG**CCCCCGGGTGGGCAGGGGTGCGCGCCGCCGTGCGCGCC
 CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCCCTGAGTGGGCCCTCCAGCGCTCGCCTGCC
 CACCAAGTGTACTGTCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCCTCCGCGCGGTTT
 CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
 ACCAAGATGGACTTCGCTGGGCTCAAGAACCCTCCGAGTCTTGATCTGGAAGACAAACAGGT
 CAGCGTATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGGACTGCGCTGAACA
 AGAATAAGCTGCAAGTCCCTTCCAGAATTGCTTTCCAGAGCACGCCGAAGCTCACCAGACTA
 GATTTGAGTGAAAACAGATCCAGGGGATCCCGAGGAAGGCGTTCCCGGGCATCACCGATGT
 GAAGAACCTGCAACTGGACAACACACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
 TCGCGCATTTGGAGATCCTTACCCTCAACAACAACACATCAGTCGCATCCTGGTCACCAGC
 TTCAACCATGATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
 CCACCTGGCCTGGCTCTCGGATGGCTGCGACAGCGACGGACAGTTGGCCAGTTTCACTCT
 GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
 TGCCACGCCCCCATCTCGGAGCCCCATCTGCAATGCCAATCCATCTCTGCCCTTCGCC
 CTGCACGTGCAGAAATAACATCGTGGACTGTGAGGAAGAGGCTTGATGGAGATCTCTGCCA
 ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAAGTCCATCAAAGCCATCCCTGCA
 GAGGCTTACCCAGTACAGAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TATTGCTCAGATGCGCTTCCAGGGCCTGAATCACTCCATCGCTGGTCTGTATGGGAACA
 AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
 AATGCCAACAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAAGCTCAACTT
 GCTCTCCTCTGTATGACAAACAAGCTGCAGACCATCAGCAAGGGCCTCTCGCCCTCTGCAGT
 CCATCCAGACACTCCACTTAGCCCCAAAACCCATTGTGTGCGACTGCCATGGAAGTGGCGTG
 GCGGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGCCGCTGCAGCAGCCGCGCCG
 ACTCGCCAACAAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCCGAGCAGGTTTACGAGCGAGTGCTTCATGGACCTCGTGTGCCCGGAGAAGTGTGCG
 TGTGAGGGACAGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC
 TGAATATGTCAACCGACTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCAACCTCGGAAAAATAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACACGCT
 GGAGACCGTGACGGGCGCGTGTTCGTGGCCTCAGTGGCCTCAAAGCTTGATGCTGAGGA
 GTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCGCGCCTGAGTTCCGTGAGACTGCT
 TCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCAACACGCTTGTCTCCCT
 GTCCACCATAAACCTCCTGTCCAACCCCTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGCGGATCGTCAGTGGGAACCTAGGTGCCAGAAGCCATTTTCTC
 AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCCGCGCTGCCCGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT
 GCAGCAACAAGGGGCTCCGCGCCCTCCCCAGAGGCATGCCCAAGGATGTACCGAGCTGTAC
 CTGGAAGGAACACCTTAACAGCCGTGCCAGAGAGCTGTCCGCGCTCCGACACCTGACGCT
 TATTGACTAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCACTAATCATGTCTC
 ACCTCTCACTCTGATCCTGAGCTACAACCGGTGAGGTGCATCCCGTCCACGCTTCAAC
 GGGCTGCGGTCCCTGCGAGTGCTAACCCCTCCATGGCAATGACATTTCCAGCGTTTCTGAAG
 CTCCTTCAACGACCTCAGATCTTTTCCCATCTGGCGCTGGGAACCAACACCTCAGCTGTG
 ACTGCACTCTTCGTGGCTGTGCGAGTGGGTGAAGCGGGGTACAGGAGCCTGGCATCGCC
 CGCTGCACTAGCCCTGAGCCCATGGCTGACAGGCTCTGTCAACCCCAACCCACCGCTT
 CCAGTGCAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCGCTTCCGCTCCAGCC
 CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTGCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTACAGCTGCTCCTGCCCTC
 TGGGCTTTGAGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACTACGTGTGTATCTGTGCCGCTAACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCCTGAGCTGAACCTCTGTGACGATG
 AGGCCAAGTGCACTCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTGT
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGGCTTCAGTGGACCTTCTGTG
 AACACCCCCCACCATGGTCTTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCGAAAC
 GGGGCCCAGTGCACTCGTGGTGACGAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCCG
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAGACTCCTACGTGGAACCTGG
 CCTCCGCCAAGGTCGACCCCCAGGCCAACATCTCCTGCAGGTGGCCACTGACAAGGACAAC
 GGCACTCTTCTCTACAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCCAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCTGAACCTAGTAGTG
 GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCTTGGCCAGGGCACGG
 ACCGGCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGGAG
 GACTTCAAGGCCCTCCACCACAGTCCCTGGGGGTGTCCACAGGCTGCAAGTCTCTGCACCGT
 GTGCAAGCACGCCCTGTGCCGTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
 GCTGGACCGGCCCACTCTGCGACCAAGAGGCCCGGACCCCTGCCTCGGCCACAGATGCCAC
 CATGGAAAATGTGTGGCACTGGGACCTCATACATGTGCAAGTGTGCCAGGGCTATGTGAGG
 GGACTTGTGTGACAACAAGAAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCCTGTGCCAGCCCGGCTTTAGCGGC
 GAGCACTGCCACAAGAGAATCCGTGCCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCTGTGGGGCT
 GTGGGCCCAAGTGTGCCAGCCACCCGAGCAAGCGGCGGAAATACGTCTTCCAGTGACAG
 GACGGCTCCTCGTTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
 C**TAA**GCCCCCTGCCCGCTGCCCTGCCACCTCTCGGACTCCAGCTTATGAGGTTGGGACAGCC
 ATGTGGGACCCCTGGTGATTGACATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA
 AGAGAATATTAAAGTATATTGTAAATTAACAAAAAATAGAAGTTAAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGI PRN
 AERLDLRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKA FRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRI LVT SFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRVTGQFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFTQYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK
 GLFDGLVSLQLLLL NANKINCLRVNTFQDLQNLNLSLYDNKLQ TISKGLFAPLQSIQTLHL
 AQNPFVCDCHLKW LADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRI PSHLPEYVTDLR LNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNTDFAGLSSVRLLSLYDNRI TTTTPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSQQLSPRCPEQCTCMETVVRC SNKGLR
 ALPRGMPKDVTELYEGNHLTAVPRELSALRHLLTLDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCD CSLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHR FQCKGPVDINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACPY SYKGKDVTPINTCIQNPCHGGTCHLSDSHKDGFSCCPLGFEGQR
 CEINPDDCEDNDCENNATCV DGINNYVCICPPNYT GELCDEVIDHCVPELNL CQHEAKC IPL
 DKGFSCCECVPGYSGKLCETDNDDCVAHKCRHGAQCVD TINGYTCTCPQGFGSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCIVVQQEPTCRCP PGFAGPRCEKITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSPPTTVYSVETVNDGQFHS
 VELVTLNQTLNLVVDKGT PKSLGLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSV VCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSVFEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

GGATGCAGGACGCTCCCTGAGCTGCCTGTCAACCGACTAGGTGGAGCAGTGTTCCTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACGGCAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAAACAACCACTGCCATGTGCGCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAATTTGTTAAAGA
GACACAAGGAATGAACATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTTCCTTAAACTGGAACGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA
TTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATTGC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
 TVLDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMN
 YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

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FIGURE 115

CAGGCCATTTGCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAACCTTGTACATGGCTCCC
 CATTTGGTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTT
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTTACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCGTGATGTCTCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCCAAGTCATTGCTGTTAATTCGGGTGGACCCCTGGAGT
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTTCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAATGTCAATTTTATGGATTGTAGACC
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTCATAGTTTAAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCACAGATTCAAAT
 CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTTGTTTGTCCCTGTCTTGGCTGGATC
 CATAGCGAGAGTGTCTGTATTTTTTTAAGATAATTTGTATTTTGCACACTGAGATATAA
 TAAAAGGTGTTTATCATAAAAAATAAAAAAAAAA

Signal peptide:

amino acids 1-15

MPLLKLHVHSGPLVFGKFKLFTLVSAIPVFRLARRRKKILFYCHFPDLLLTKRDSFLKRLY
 RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
 DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
 HYQELKKMVQQSDLGQYVTFLRFSFDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
 IAVNSGGPLESIDHVSVTGFLCEPDPVHFSEAIKFIREFPSLKTMTGLAGRARVKEKFSPEAF
 TEOLYRYETKLHV

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATG**TTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGAAAAAGGCTTTCTAGATGGGTACAC
 TTGATAAAAACATGACTCGGAAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTGTGCATAATAACTGCAAAAATTGTGTACCTGGGCAATCTGTTTTTAAACCACCTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTTGTGAAACTGTTGCAACTGCCA
 AACTGACTCCAGTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATT
 CCTAGAGAGACCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTTCCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAAGTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 AT**TAA**ATTTTATACATTTAAATCATTTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVSLGTVDLVKQHINPNKTSDPFETMLKSLRLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLLLKSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTVWSEIGKGFLDGS�DKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLTTSSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLVYALGVVL
QDPNTWPSPHKFPDRFDDELVMKTFSSLGFSGTQCEPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA
 GACCGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTCCTCTCGCTTC
 CTGACGCTCCTGGCGCATCTGGTGGTCTCATCACCTTATTCTGGTCCCGGACAGCAACAT
 ACAGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTACAGCTGG
 TGGCCGCGCTCTCTGTCAACCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
 GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
 GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTGTCT
 TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTACCGTCTTTGGGCTGAAA
 AAGAAACCCCTTCTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
 CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
 TGCTGGAGGATATGTGTGGAATAATTACGCTCTGAGTCTGGGATTATCCGCATTGTATTTA
 GTGCTTTGTAAATAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTtaggggaca
 ATTAAAAAAAAAAAA

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MGRVSGLVPSRFLTLAHLVVTITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

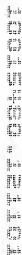


FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
 CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
 GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
 ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC
 AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC
 AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC
 CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
 ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
 CAGGGAGCCCTGAGGTCCAATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
 TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TG**AGGCC
 CTGCTGATCCGCACCCCATTCCTCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
 ATAAAGATGTAGCTC

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FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
 AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
 MSIGISFMGNMYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
 IQNWPHYRSP

Signal peptide:

amino acids 1-20

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
 AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
 MSIGISFMGNMYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
 IQNWPHYRSP

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCCCGGCTCAGAGGACCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCTCGGAAGCGGGGCCACATCTACCTAAGTCCGCCCCATGGCCAATTCCACTCT
 CCTAGGGTGCTGCCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC
 TGGG**TGA**CCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCCTCAGGCAGGAGGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCTCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCTCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCTTGAGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCTTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCC
 ACAGCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTACAGCCGGGGTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGCGGGGCCGGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGAAGTCTGTG
 GAAACCGTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGAGCAGGAATAAGCTT
 GCCCCGGGGCA

0-15
 16-31
 32-47
 48-63
 64-79
 80-95
 96-111
 112-127
 128-143
 144-159
 160-175
 176-191
 192-207
 208-223
 224-239
 240-255

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLLVICQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGR
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPY
YPSG
```

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACAGAGTGGGTGCAGGGGCCCCA
 GGCAGGGTGATTCTTTGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
 GACAAAGTTAACAGAGCCAGCGAGAGACTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTCTGACCTAGCCGCTAG
 CATCTTCCCGAGCACCCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGACCAGCGCCAGCC
 GGTGCGGCTGCCACACGGCTCACC**ATG**GGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCCCTACGCTGCCGGGGCTGCCCGCTCTGGGCACAGAACGACACGGAGCC
 CATCGTGTGAGGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGTGCCTTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCCTGGTGAATGTGGTAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA
 GAAAAGGAATTTACAGTTTCAGTTTTTCACGTGATTAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACAGTAATATCTGCCCTTTCGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG
 TTCCCCCTA**TAG**GATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTCACAGATTATTTGTG
 TGTGTCTGTTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAGCTGTCTGCAAGACTTATCTGAATTTCAATTCCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTAAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGGTTTGGTTCTTGTA
 AAAACTTGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGCTTGCCCACAAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAAATGTATATGTGAAGAGTCATATTTTCCAAGTTATATT
 TTTCTAAGAAGAATAGATCATAAATCTGACAAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAATCTTATACCTTTATGTC
 TCAACTTTAATTAAATGATTGATAATAACCACCTTTATTAATAAACCTAAGGTTTTTTTTTTT
 TCCGTAGACATGACCACCTTTATTAACGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATGTGA
 TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTTGCTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAA

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCCTGCGCTC
GCCCTTTATGTCTTACCATCGCCATCGAGCCGTTCGATATCATCTTCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTCGTCCCTTGTTGGTTCATGGCAAGAGTCATT
TTGACAACAAGATGGACCAACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAAACCCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCTCAATTCTTCTTTATTACAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTCTTATTATGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGACACTTTCCTTTTACAAGCAGCGCTCCAGATTAACCTCAGGGAACAGCACTTCCCAA
ACCGCAGACTACATCTTTTAGAGGAAGCACAACTGCGCTTTTTCTGAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAGAACTATGCAGATA

FIGURE 128

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPQTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLG
GIMSGVFSFVNTLSDSLGPGTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKK
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN
FLLYNQRSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACAGCGCCGCCACCCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTGGCTCTCGGCGCTTGCCCTTTCT
 TGGTGTCTTGGTGGCTCGGTGCTGAGAGCCATCTGGGGGTTCTGGGCCCCAAGACCGTCTCGCAGAAAGACGCCG
 AGTTTGGAGCCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTCAACCATCTGTGACCC
 GCAACAGGACAGAGGGCGCTGTGTCTGTGAACGTCTGAAACAGCAGAGGGGGGCCGCTGTGTGTTTGTGG
 TCCGCCAGAAAGAGGCTGTGGTGTCTTCCAGGTGCCCTTAATCTCGAGAGGATGTTTCAGCGCAAGTACCTCT
 ACCAAAAGTGGACGAACCCCTGTGTGAGCCCCACCAAGAATGAGTCGGAGATTCACTTCTCTACGTGGATG
 TGTCCACCTGTCAACGAGTCAACACCATACCACTCCGAGTCCGGGTGAGCGCATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTCAGCTCTCAATACACAGCAGCAGCCCGAGTACTTCAAGTATGAGTTCCTCGAAGCGGTGGACT
 CGGTAAATTGTCAAGGTGACCTCCAAACAGGCCTTCCCTGCTCAGTCATCTCAATTCAGGATGTGTGTGTCTGCT
 TCTATGACCTGGACAAACAGCTAGCCTTCTATCGGCATGTACAGACGATGACCAAGAAGCGGCCATCACCCGTAC
 AGGCGAAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGAAGACCAGAGACCAAGCCTCGGGGGGCT
 CCCTGCTTTTCAACCCCTTCGACAGAGATGACCCGGTGCATCAAGGGCACCGCCAGAAAAACCTGTGAGTGTCTG
 TGTCTCAAGCAGTCACTCTGAGGCATACCTCAGTGGGATGCTCTTTTGCTGGGTATATTTCTCTCCTTTTACC
 TGTCTGACGCTCTCTGGCTGCTGGGAGAATGGAGGCAGAGAAGAACCCCTGCTGTTGGCCATGACCCGAG
 CTTGCCCAAGAAAGCGGTCAACCTCGAGTCTGGTGAATCTTTCTCGCAGITCCCTTTATGAGGTTTACAAC
 ATGCTCCTGTTGGAATGTTCTTGATCTACCCAGTGGTGTGTTGACAGCGCTGGACATGGGACCTCTCTTACG
 GTACCGAGCCGCTCTTTTGAACCTTAGGTACTCGGCCCGAGTGGACTCCATGAGCTGTGTGGAGGAGGATG
 ACTACGACATGTGACCGCATGTCATTCCGACAAAGATGTCTTTCGACCAAGCAATACCTCTGTGTGGCTGACC
 TGGCGAGGAAGGACACCGGTGTTCTGGGAAAAAGTACCAAGTCTACTTCTGGAACATTGCCACCATGTCTGTCT
 TCTATGCCCTTCTGTGGTGCAGTGGTATCACTACAGACGGTGGTGAATGTACAGAGGAATCAGACATCT
 GCTACTCAACTCTCTCTGGCCCAACCCACTGGGCAATCTCAAGCCCTTCAACAACTCTTCAACAACTCGGGGT
 ACATCTGCTGGGGCTGCTTTTCTGCTCATCTCTGCAACGGGAGATCAACCAACACCGGGGCTGCTGCGCA
 ATGACCTGTGTGCCCTGGAATGGGATCCCAACACTTGGGCTTTTCTACGCCATTCGACAGCAGCCTGATGA
 TGGAGGGGCTGCTCAGTGTCTGCTATCATGTGCCCCAATATACCAATTTCCAGTTTGACACATCGTTTATGT
 ACATGATCGCGGACTCTGATGCTGAAGCTCTACCAAGCGGACACCGGACATCAACGCCACGCCCTCAGTGT
 CCTACGCTGCTGCCATCGCATCTCATCTTCTTCTGTGTGCGGCTGGTCTTTTGGCAAGGAACACCGCGTCTT
 GGATCGTCTTCTCCATCATTCATCATCGCCACCTGCTCCTCAGCAGCGAGCTCATTTACATGGGCGGTGGA
 AACTGACTCGGGGATCTTCGCGGCACTCTCCACGTGCTCTACACAGATGCATCGGCGATGCAGCGGGCCG
 TCTACCTGGACCGCATGTGCTGCTGTCATGGGCAACGTCATCACTGTGCTGCTGCTGCTTACCTGGGCTTATCA
 TGGCCCCCAATGATTTCGCTTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCTTTTACTTCGCTTTTACA
 TCTATCAAGCTCCGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTGTGATGTTTGACACTCCGTTGGTCT
 GGGCTTTCGCTCTTCTCTCTTCCAGGACTCAGCACTGGCAGAAAAACCCCTGAGAGTGGAGGGAGCACA
 ACCGGGACTGCATCTCTCGACTTCTTTGACGACCAGACATCTGGCAGTCTCTCTCTCCATGCCATCTGTCG
 GGTCTTCTGCTGGTGTGTGTGACACTGGATGACGACTGGGATCTGTGACGGGGACAAGATCATGTCTTCTAGC
 AGGAGCTGGGCGCTTCGCTTCACTCAAGGGGCCCTGAGCTCCTTTGTGTATAGACCGGTCACTCTGTCTGTCT
 GTGGGATGATCCGACGACCGCTGCCAGCACTGGATGGCAGCAGGACAGCGAGTCTAGCTTAGGCTTGGCT
 GGGACAGGCATGGGTTGGCATGGAACCTTGCAGCTGCCCTTCTGCCAGGAGCAGGCTGCTCCCTCGGAACCCG
 AGATGTGGCCAAATGTGCTCTTCTCTCAGTGTGGGGCTTCCATGGGCGCTGTCTTTGGCTCTCCATTT
 GCTCCTTTTGAAGAGGAAGGATGGAAGGGACACCTCCCATTTATGCTGCTGATTTTGGCGTCTCTCTCCCC
 ACAATGCCAGCTGGACCTAAGGCCCTCTTTTCTCCCACTCCCACTCGGAGGCTAGTCTGGGGCTCTGA
 ATCTCTGCTGTATCAGGGCCCCAGTTCTCTTTGGCTGTCCCTGGCTGCCATCAGTCCGCATTCAGCTCAGCC
 AGGATGGATGGGGTATGAGATTTTGGGGTTGGCCAGTGGTGCAGACTTTTGGTGTCTAAGCCCTGCAAGGG
 CTGGGGCAGTGGCTATTCTCTCTGACTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCAAAT
 TGAAGACCGCTCTGATTCAAGAGGCTGAATCAGAGTCACTCTTCACTCCAGTCAAGCTGATGCTGCC
 AGCAGCAGGATGGAGGGAGAGCGCTCACCCCTCCCTCTCTTCTTCCAGGCGCTTAGTCTTGCACAAACCC
 AGCTGTGGGCTTTCAGTGGCTGACATGCTGCCAAGAATGTCCAGGGGCAAGGGATGATACAGAGTTACG
 CCGTCTGCTCTCCAGCTGTGGGACCCAGTGCCTACCTTAGAAGGGGCTCAGGAAGGGATGTGCTGTGTT
 CCTCTACGTGCCAGTCTAGCTCTGCTCTAGGACCCAGGGCTGGTCTTAAGTTTCCCTCAGTCTCAGGCA
 AGTTCTGTGTAGTCAATGACACATACCTATGAAACCTTGGATTTTACAAAGATTTGCCCGAGCTCTGGGCA
 CTGGGCCACCTGGTCTTGGATCCCCTTCTGCTCCACCTGCTCAACCCAGTGTGAGGATGTGAGGGAGCTCAGG
 CGGGGCTCTGCTTTGGGATGGGAATGTGTTTTTCTCCCAACTGTTTTTATAGCTCTGCTTGAAGGGCTGGG
 AGATGAGTGGGTCTGGATCTTTTCTCAGAGCTCTCCATGCTAGTGTGATTTCCGTTTTCTATGAATGAAT
 TGCATTCAATAAACACAGACTCAAAAAA

FIGURE 130

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPLVLVLLVASVESHVGLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVNLNKKQKGAPLLFFVVRQKEAVVSFQVPLILRGMFQKYLQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQPQYFKYEFPEGVDSSI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTLVSVLSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVLAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDSL SYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDS DKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGFLFYAMGTALM
MEGLLSACYHVCPNYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKNTAFWIVFSIIHIIATLLLLSTQLYMGWRKWLDSGIFRRILHVLVYTDICIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF

```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCCTGCGCTTGCCCCACCCAGGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGCCAGCTGGACCAAGGGAGGCCAGTCTTGGGCGCTGGAGGGGCTGTCTTG
 ACCA**TGGT**CCCTGCCTGGCTTGGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC
 CCAGCTTGACAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACCC
 TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGTGTGAGGGGACTCA
 GGCAGGGCAACTGAGGGCCATTTGCTATGGATCCAGATTCTGGCTCCTGCTGGTGACCA
 GGCCCTGGACCCAGAGGAGGACGGCAGAGTACCAGCTACAGGTCAACCTTGGAGATGCAGGATG
 GACATGTCTTGTGGGCTCCACAGCCTGTGCTTGTGCACGTGAAGATGAGAATGACAGGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCCTGGCATCCC
 CTTCCTCTTCCCTTGAGGCTTCAGACCGGGATGAGCCAGGCCACAGCCAACTCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACACGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCCTCAGGCCACCCAGGCCACTG
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCCTTAGAGCCTATCCACCTGGCA
 GAGAACTCTCAAAGTCCATATACCCGCACCATGCCCCAGGTACACTGGAGTGGGGGTGATGT
 GCACATCTCACCTGGAGAGCCATCCCCGGGACCCCTTGAAGTGAATGCAGAGGGAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCTTGGCGAGGACTATGCGGCCCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACTGCGCTATCTGCCCTCCCCGTGACCCCAAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTC
 CAGCTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
 GGTGGACCCCACTTCAGGCACTGTGACGCTGGGGGTGCTCCCATCTCCGACAGGCCAGCAACA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGAGTCCACAGATATCAATGATCACGCCCTGAGTTCACTTCCAGAT
 TGGGCTATTAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCTTCCGCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCACGCCCTTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCC
 AGCCGGCTCTTTCCTGCTGACCATCCAGCCCTCCGACCCATCAGCCGAACCTCAGGTTCT
 CCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATCTCCCGGGGAGGTGCACACC
 GCCAGCTCCTGCAAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCAGGA
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCCAAGACCATG
 GCTTGCTGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
 TTCACCTTGGTCCCCACCCACGGTGCAACGGGATTTGGCGCTCAGACTCTCAATGGTTTC
 CCATGCTTACCTCACCTTGGCCCTGCATTGGGTGGAGCCAGTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGCTGCTGCAAC
 GTGGAGGGGACGTGCTATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAGCTGTGCGG
 AGTGGGCATCCTTGTAGGCCACCTGGTAGCAATAGGAATCTTCTCATCTCTCATTTTACCC
 ACTGGACCATGTCAAGGAAGAGGACCCGGATCAACCAGCAGACGCTGCCCTGAAGGCG
 ACTGTCT**GAA**TGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGGAGCCAGCCCAAGATCCAGAGGGGACAGGACAGGATGAGAAGCCCTCCAT
 CTGCCCTGGGGTGGAGGACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC
 TTTATGGACTGCCCATGGGAGTGTCCAAATGTGAGGGTGTGGCCCAATAATAAGCCCCA
 GAGAAGTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSPQALPKAQAELSVVEVPENYGGNFLLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGFQPVLVHVKDENDQVP
 HFSQAIYRRLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSI IESTWVSLEPIHLAE
 NLKVLYPHMAQVHVHSGGDVHYHLESHPPGPFVEVNAEGLYVTRELDREAQAQYLLQVRAQN
 SHGEDYAAPLELHVLVMDENDNVPICPPRPDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAQVDPSTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGLVAMLTADADLEPAFRLMDFAIERGDTE
 GTFGLDWEPDSGHVRLRLCKNLSYEAAPSHEVVVVQSVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPI SAPAGSFLLTIQPSDPI SRTLRFSLVNDSEGWLCIEKFSGEVHTA
 QSLGQAQPGDITYTVLVEAQDTALT LAPVPSQYLCTPRQDGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRLQTLNGSHAYLT LALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTTLVAIGIFLILIFTHWTMSRKKDPDPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTGCAGAAATGGAGACGAGATCAGCAA
 ATTTGAGTCAACTAGTGAATTCAAAACAACCTGAAAGCTCAATTTCTGGAAATCTCCCTCCTCT
 TCAATCGGCCTGTGGATGTCTGTGCCATCTGTCAAGTCTGCAGGCATTTAAATCCTTCTCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAAATGCAACACATATGAAGGGCAAGAACCGGACGATTAACATCAACTACCGGGG
 CTTACCATTTCCCTGGAAGCTATTTACCACGAGATGGACAACATTCGCCGAGACTTTCTTGAC
 CTGGCGAGGAGGTGAAGATTTGGACATTCGTTTGAAACCGGCCGATGTATTACTGAAGTT
 CAGCACTGGGAAAGGCGTGAGCGGCCGGCCGCTTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTTGGAGAAAATGGATATTTTCTTTGTGCCTGTGGCCAATCC
 TGATGGATATGTGTATACTCAAACCTAAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG
 GGAGCCAGCGACAACCCCTTGCTCCGAAGTGATACCATTGGACCCACGCCAATTCGGAAGTGA
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCCAGCTCG
 ACAGCTACTCGCAGCTCTGTATGATATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTCGGGCACTGA
 TACCAAGTGGGTCCCACTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAACGGCATCAAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC
 TTCCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGCGCATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTCCCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGGAT
 CGTGTGCTCTGGCGGTGTCCTGCAAGAACTGGTTCTGCCAGCTGCTCAATTTTGGTCTCTG
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC
 AGCATCACCCCTTCTCTGGGTGGCATGTCTCTCTTACCTCATTTTTAGAACCAAAGAACATC
 TGAGATGATTCTCATCCCTCATCCACATCTAGCCAAAGCCAGTGACCTTGCTGTGGTGGCACT
 GTGGGAGACACCACTTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCCCTTTAATTT
 TCGCAGCTCTTCTCGAAAAATATTTTCTTTGAGCAGCAAATCTTGAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCCTCCTGTTTTTTTTTTTTTTTGGAGACAGATTTTGTCTTGTGTGCC
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCCTCCTGGGTTCAAGCA
 ATTCTCCTGCCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCGGCTA
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCCGTCCCTCCTTTTTTAGGCCCTGAATACAAAGTAGAAGATCACTTTCCCTTAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTATTACGTGTG
 ACCAGGATGGCGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTCAGGATGGTGAATATCCCCATCTGTCTAATGGGCTTACCTCCT
 CTTTGGCTTTTGAACCTCACTTCAAAGATCTAGGCCCTCATCTTACAGGTCCTAAATCACTCAT
 CTGGCTGGATAATCTCACTGGCCCTGGCACATTCCCATTGTGCTGTGGTGTATCCTGTGT
 TCCTTGTCTCGTGGTTTGT
 TCTGTCTATTTGTATCTGTGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT
 GCCTCTGTGTTTGTCTTCACTCAGCACGTACCATCTGCTCTTTGTGTGTGTGTGTGTGTGT
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAAATCTTAACCTCCTGCCCTAGGATTTGTACA
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFN
 PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH
 SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
 SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
 SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY
 SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
 NGIKFAFTFELRDTGTYGFLLPANQIIPTAETWLGLKTIMEHVRDNL

Signal peptide:

amino acids 1-16

[illegible]

FIGURE 136

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
 TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP
 SKDLTLKMGSALFVKKEQLQANFLGNVKKRYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
 VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
 GVDTELNCFVLQMDYKGDVAFFVFLPSKGMQRLEQALSARTLIKWSHSLQKRWIEVFIPRF
 SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
 KFIVRSKDGPSYFTVVSFNRTFLMMITNKATDGI LFLGKVENPTKS

Signal peptide:

amino acids 1-20

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FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSSVISSGASTATNSGSSVTSSGVSTATI
 SGSSVTNNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSE
 SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
 TTSSGASTATNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTT
 SNGAGTATNSESSTSSGASTATNSDSSTVSSGASTATNSESSTSSGASTATNSESSTSS
 GASTATNSDSSTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTSSGA
 NTATNSESSTVSSGASTATNSESSTSSGVSTATNSESSTSSGASTATNSDSSTTSSEAST
 ATNSESSTVSSGISTVTNSESSTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
 SEAKPGGSLVPWEIFLITLVSVVAAGLFFAGLFFCVRNSLSLRNTFNTAVYHHPHGLNHGLGP
 GPGGNHGAHRPRWSPNWFWRFPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
 CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
 CTGCTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
 ATGCCGGAAGGGGAAGTGGAGAAGGTTTTC AACGGA CTAGCAACATGGGGAGCCACACCGGC
 AAGGAGTTGGACAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCACACTGGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
 GGCTCAGTCAACACGCCTTTCATCAACCTTCCGCCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCTTAAACTGGCATCCGGCCTTGTCTGGGAGAATAATGTCGCCGTTGTGACATCAGCTGAC
 ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTG
 GGATTGTGAATAAACTTGATACACCA

FIGURE 140

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

CC CGGGT CCCAGGGGGCT CGCG CGGGCG GGGCTGG CAAAGGGGGAGCAT AGT CAGTGGACAT CCAAGGAAGCGCGG
CCCGCGGGGGGACAT GACCTCGGCTGACCTT GACTACT CTAAGTTCGCGAGGCGGGGGCCCCCGGGGCGACTCG
GGGGCGGACACCGGGGGCGGAGT CGCGCCCGT GAGTTCGCGCGAGGCCAT CAGTACCGCGACGCCCGCGGACACCGCTG
GCTCTGCTCTCTCGAATGCTCGCAGCGGATGGGCTCTGAGAGCTGGCTCGCGCCCCATGGGGCGCGCTCGCG
CTCGGCCACCGCTGCTGCTGCTCTGCTGCTGCTGCTCTGCTGCAAGCCGCCCTCGAAGCTGGGCGCTCAGC
CCCCGATCAGCTGCTGCTGGGCTCTGAAGAGGGGCCATCTCTCAGATTGGAAGTGTGACACATCTCCAATC
ACAGCCGCTTCTGCTGACAGGGATGCGAGGCCAGCTGTACGTGGGTCTCGAGAGGCCCTCTTTGCACTCAGTAC
AACTCAGCTTCTCTCGCAGCGGGGAGTACAGAGAGTCTGCTTTGGGTGAGACGCCAGCAAAACACAGTCTG
AGCTTCAGGGGCAAGGACCAACAGCGGCTATCTCAAATACATCAAGATCTCTCTCGCCTCAGCGGCTCAG
GTGTTCACTCTGGCAGCAGCTCTGACCCCATCTGTACTATACATCAACATGAGAACTTCACTGGGAAAC
GACGAGAAGGGGATGTCTCTCTGGAAGATGGCAAGGCGGCTCTCTCCCTGCAAGCGAATTCAGTCTCACTGC
TGCTTGTTGTTGATGGGACGCTCTACATCGAAGCAGTCAGAGCTCTCAAGGAATGAGCGGCCATCTCGGAGC
CAAAGCTCTCGCCCAACCAAGACCGAGAGTCTCCCTCACTGGCTGCAAGACCGAGCTTTTGTTGGCTCAGCTAC
ATTCTGTAGAGCTCTGGGACGCTGCAAGGCGATGATGACAGATCTACTTTTCTTCAGCGAGGATGCGCAGGAA
TTTGAGTTCTTTGAGAACCACTTGATGCTCCGCTATGTCGCGATCTGCAAGGCGGCTGTCAGAGGCTGAGAGCGGGTG
CTACAGCAGCGCTGGACTCTCTCTCTCAGGGCCAGCTGTGCTGTGCTGACGCCCGACAGATGAGCTCTCCCTTCAC
GTGCTCGAGATGATCTTCAGCTGTGAGCCGCCGCCAGGACTGGGCTGACACCCTTTTCTATGGGTTTCACT
TCCGCTGTGGCAGAGGAACTACAGAGCTCTCGCGCTTGCTGTCTCAACAAGAAAGTTGCGAGAGAGCTTC
AGCGGCTCTACAAGAGGCTGAAACGCTGAGACAGCAGTGGTACACGCTGACCCACCGGTCAGCCAGACCCGGG
CTCGAGGCTGATCATCAACCAAGTGGCCGGGAAGGAAGATCAACTCATCTCTGCACTCCAGACCGCGGCTGTG
AACTTCTCTAAGACCATCTCTGATGACGGGCGAGTCCGAAGCGCATGCTGCTGTGACGCCCGAGGCTCG
TACAGCGCTGCTGCTGTACACCGCGTCTGGGCGCTGACCAACCACTACGATGCTCTCTCTGGGCACTGTGAG
GGCGCGCTCTCAAGGACGATGAGGCTGGGCGCCCGGGTGACATCACTGAGGAGTCGACATCTTCTCATGGGA
CAGCCCGCTGCGAATCTGCTCTCGGACACCAACGGGGCTGCTGTATCGGGCTACACTCGGGGCTGATCGAG
TGTCGCATGGCAACTGCAAGCTGTACCGAGCTGTGGGAGTGGCGTCTCTCGCCGGAGCCCTACTGTGCTGG
AGCGGCTCCAGCTCGAAGCAGCTGAGCTCTACCGAGCTCAGCTGGCCACAGGCCCTGATCCAGGAGATCTGAG
GAGCGAGCGCGCAAGACCTTTGACGCGGCTCTCGGTTGTGTCGCCCTCTTTTGATACCAAGGAGGAGAACCA
CTGTGAGCAAGTTCAGTTCCAGCCCGCTGAGCAGTGAACTATTTGGCTCTGCCCTCTCTCTCCAACTCGGCGACCGA
CTCTGGCTACGCAAGGGGCGCCCGCAATGCTCTGGCTCTGCAAGTGTCACTCACTGGGAGGACTGTGTGCTG
GTGGGCAACCAACAGCTGGGGAGTTCGAGTCTGCTGCTCACTAGAGAGGGCTTCACGACGCTGGTATGAGCAGCTAC
TGCCAGAGGTGTGTGAGGACGGGGTGGCAGACAAACAGATGAGGTGGGAGTGTACCGCTCATCTTACAGTCA
TCGCTGTGTAGTGCACAGCTGTGTGCGAAGGCCACTGGGGTGCAGACAGTCTCTATGGAAGGAGTTCTTGTTG
ATGTGACGCTCTTTGTGCTGGCGCTGCTGCTCCAGTTTATTCTTGCTTACCGGCAACCGGACAGCATGAAA
GTCTTCTCGAAGCAGGGGATGTGTGCAAGCTGCACCCCAAGACTGCGCTTGTTGTGCTGCCCTCGAGCCGCT
CACTCAACCGCTAGGCGCCCTTAGCAGCCGCTGTGATACAGGAGGTACAGTCCCTGTGACAGACGCCCGCG
GGGGCCCGAGTTCTTCTAGTGTACAGAGAAGAGGCCACTCAGCATCAAGAGAGCTCTGTGGAGGATATCCCAAGT
TGCCCCGGCCCGGGTCCGCTTGTGCTGGAGATCGTGTACTCTGTGCTGTCAGAGGCTGACTTCCAGAGAGCG
CGCCTTGCTTCAGGGGCTGTGAATGCTCGGAAGAGGCTCAACTGGACCTCCCTTCGCTGCTGCTCTGTCTGGAAC
AGACCGTGTGTGCGGGCCCTTGGAGGCTTGGAGCGAGTGGCCTGTGCTGCTCTCAGTCAAGTGAAGAGCTCC
TACACCCCAACACCAACCAAGCCGTGGCCCGAGAGTCTGTGCCCAAAATATGGGGGCTCGCTAGTGTGTGAA
CAGTGCTCTTATGTAAACTGAGCCCTTTGTTTAAAAAACCAATCAAATGTGAACTAGAAATGAGAGGGAGAG
ATGAGTACAGCATCAGCAGCAACCGGCTGCTPCAGTTCTATGGCTCTCCAGGGGTCTGGGAGTGCATCAAAGTGG
TTGCTGAGACAGATTTGGAACCTCTCAACACTGGCTCTTCACTCTCCAACTTCTCCGCTGCACCCGGCTGCG
CTGTCCTCAGTCAGATTCAGGACAGGCTTGGGCTGGTGCGTGTGCTGCTGCTGCAAGTCAGCGAGGATGTAGTTG
TTGTGCTGCTGCTCGTCCCAACTCAGGAGCAGAGGGCTAGTTTGGCATCGGGCCCTACAGGTCCTGGGCTC
GGACCAACTCTTGAGCTTTCCAGCTGTATCAGGCTGTGGCCACAGCAGGATACGCGGAGCTCAGGAGAAGA
TTTGTGGAACCTGTGAGCTCTTCTCTCAGAAATCAGGGAAGAGCACTGCGGCTGCCCTCTCTCGTTGTGCTGTA
GAAACCGTGTGCCCTCTCCCACTATCAACCTCGCTCCATCTTTGAATCAAAACAGGAACTAATCGACCC
GTGTCCTCTCCCGAGTCCGAGTCACTCCCTCCCTCCTCACTTCTCCACTCAAGGATATCAACACTGCC
AGCAGAGGGGCCCTGAATTTATGTGGTTTATTATCATTTTAAATAGATGCATTTATGTCAATTTTAAATAAA
GTCTGAAGAATTACTGTTTAAAAAAAATAAA

FIGURE 142

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSLAAPWGALPPRPPLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFPLRF
EAEHISNYTALLSRDGRITLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLEEDKGRCPE
FDPNFKSTALVVDGELYTGTVSSFQGNPAISRSQLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLLQQRWTSFLKAQLLC
SRPDDGFFPNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSSGSSCKHVSILYQP
QLATRPWIQDIEGASAKDLCSASSVSPSFVPTGEKPEQVQFQPNVTNLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYKFEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECAVHPKTCVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

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Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTTGCGGCGCGCGGCTACGAAGAGGACGGGGACGGGCGCTGCGAACCGA
 GCCCAGCCACCGGAGGAGCGGGGACGGGCGGGAGCGGGAGCTCGTCTGCGCCGCGCCCTCGTGCCTGCG
 TGCCGCGCCCGCGCTCCCGCGCGGAGCGGGAGCGCGCCGACCTCGCGCCGAGCGCGCTAGCGCGCGCG
 CGGGCATGGTCCCTCTTAAAGCGCAGGGCCGCGCGCGGGGCGGGTGTGCGGAAACAAGCGCGCGCGGG
 CCTCGGGGCGCTCGGGGGCCCGCATGGGCGCGCGGGCGCGGGCTCCGAGCGCGCGCGCTGCGCGGCGCGGCTCG
 CGGCGCTAGGGCGGGCTGGCTCTCGTGGGCGGGGCGAGCGGGCTGAGGGCGCGCGGAGCTGCGGGCGCGGGCG
 CGCGCGCGCGCGCGCGCGCGGGGAGCGCGCGGGGCTAGGGCGCGCGCGCGCGCGCTGGCTCAGCGTGC
 TGCTCGGGCTCGTCTGGGCTTCTGCTGGCTCGCGGCTCGTCTGCGCCGGGCTTCCGAGCTGAAGCGAGCGG
 GCCCAGCGCGCGCGCGCGCGCGGGGCTGCGGCTCCGGGACGGCGCGGCTTCCGAGCGCGCGCGCGCGCG
 GCGATGCGCGCGGGGCGAGCTCTGGCGCGCGCGCTCGGACCGAGATGGGCGCGCGCGAGCAGGAATCTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGGTGGCGCCTACAGAACATGGTCCAAAGACA
 TTCTCGGAAAGTTCAAGTCTTCTCAAGTGAGGGTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG
 GTGTGGAGACTCTACCGCGCCCGAGAAGTCTTCAATGATGCTCAAGTACATCACGACCACTACTTTGGACA
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAGGAGACCGCTCTGGAGAACTTCTGAGGAGTT
 TGAACAGCAGCGAGCGCTCTTCTTGGGCAGACAGGCTGGGCGACCGGAAGAAATGGGAAACTGGCCCTGG
 AGCTTGGTGAAGATCTTGATCGTGGGGGGCTGGCGTGATCATGAGCGGGAGTGCTTCGAGAAATGGTGGCCG
 ACATTGGCAAGTGTCTCCGGGAGGTGACACCACTAGGAGCTGGAGTGAGGAGGTGTGTCCGAGGTTTGG
 CAGGGGTGCGATGTCTCTGGCTTATGAGATCGCGCAGCTTTTATGAGAATTACGAGCAGACAAAGAGGGGT
 ACATTAGAGATCTCCATAAGCAAAATTCACCAAGCTATCACATTACGCCCAACAAAGCCACCTTACCAAT
 ACAGGCTCCAGCAGTACATGCTGAGCGCGAAGATATCGAGCTCGCGCATCGCAATACAGCTGACCGCGAAA
 TTGTCTGATGAGCAATACAGCAACACAGAAATTCATAAGAGGACCTCCAGCTGGGAATCTCTCTCTTCTTCA
 TGAGTTTTCAGCCCGCTCGAGGAGAGGAGATTCTGGAATGGGAGTTCTGACTTGGAAATACTTGTATTTCGCGAG
 TTGAGCGCCAGCCCGCTCGAAGCGGGAATGSACTTCGCGCCAGAGGAGGACCTTGAGACGATTTGATGCAAGTGA
 TGGAGATGAATCAATGCCAACCGAAGACAGAGGGCGCATATTGACTTCAAGAGAGATCCAGTACGGCTACCGCC
 GGGTGAAACCCATGATTTGGGCTGTGATCACTCTGGACCTGTGCTCTTCAAGAAAGCAAAAGGAAAGGAGAC
 TGACGCTCCCTGTGAGGAGGACCGCTATTTCACGACAGCTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAG
 TGGATGCACAAGATTTGGCCAAAGAAATCAATCAGAAATCTGGATCTTGTCTCTTCTCAAACTCCCTGAAGA
 AGCTCGTCCCTTTTCAGCTCCCTGGGTGGAAGTGAAGAGTGAAGCAAGAAACCAAAGTAAAGATATAACATCTGA
 TTCTCTTTCTGGCGCTTTCACATGTTTGTGAGATTTATGGAAACTTTGAGAAGAGCTGTCTTATCCCAATC
 AGAAGCTCAAGCTCGTGGTCTGCTTTTCAATTTGACTCCAAACCTGACAAGGCCAAACAGTTGAAGTATGA
 GAGATTACCGCATTAAGTCACTAAAGCCGAGCATGAGATTTTGCTGTGTCTGGAGAGTTTTCAGAGCCCTGG
 CCTGGAAGTAGGATCTCCAGTTTAAACAATGAATCTTGTGCTTCTTCTGCGAGCTCGACCTCGTGTTTACTA
 CAGAATCTCTCAGCGATGTGAGCAAAATACAGTTCTGGGCGCAACAAATATATTTTCCAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATAGTGGAAAGTTCCAGTGACAACCAATTTGCGCTTACTCAGAAAAATGGCTCT
 GGAAGAAATATGGGTTGGCATCACGTGATTTTATAAGGAGATCTTGTCCGAGTGGGTGGCTTGTATGTTTCCA
 TCCAGAGGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCGAGGTTTGAAGAGCTTTTAGAGCG
 AGGAAGTAGGAGTAGTCCAGCTCCACCATCTGTCTTTGTGATCCCAATCTTGACCCCAACAGTACAAATGT
 GCTTGGGCTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGAAAAAATGATCCAA
 GTTACAGTAAAGCAGCAATAAATAGGCTCAGTGAGGACAGCCTAATGTCCAGCTTGTGTGAAAGAGCTTTT
 TAATTATCTAATTTATTTTCAAAAATTTTTGTATGATCAGTTTGTGAAGTCCGATACAAAGGATATATTTAC
 AAGTGGTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTGTGCTTTGAA
 CAGATCTCTTGTGAACATTATGACGAGACTGCTTAACCTTTGACTTGAATATGACCTGATGAAACAAACTTT
 TTTAAAAAATGTTTCTTTTGAAGCCCTTTGCTCCAGTCTTATGCGAAGAAAGCTGAACTTCTGCAAGAGTAT
 TATTGTTACAAAAACATGTAACTCTGGTAAATGTTCTGTTGTGATGTTTAACTTCCACAGATTCTACCTTTGT
 GTTTTGTTTTATTTTACAATTTGTTTAAAGCCATTTCATGTTCCAGTTGTGAAGTAAAGAAATGTGATAATA
 CTGTGTTTCAATATGTCTTCAGGAGAGCTTTCCAGAGTTGTATCTTCTCTCATGGTATCTGTCTCAGCATGGC
 CAGCTAGTGTTTTGTGTTTGTGTTTGTCTTTTGTGAGACGAGTCTCACTCTGTTTACCGAGGCTGGAGTG
 CAGTGGCGCAATCTTGGCTCACTTTAACTCCACTTCCCTGGTTCAAGCAATTCCTGCTTGGCTTCCCTCGCAT
 AGCTGGGATTACAGGCACACACCAACGCGCCAGNTAGTTTTTGTATTTTGTAGTGAAGCGGGGTTCACCAT
 GCGACGCCAGCTGGCCAGCTAGGTTTTTAAAGCGGGCGGTGAAGAAGCAGCAGGATATTTGCGTGTCTG
 TGTGATTCTGAGTCTCGGCTAATAAGACCTGGCATTAATTTCAAGAGGATTTGGCATTTCTGCTCTTGGCCCTT
 CTGTTTAAAGGGTAAAAATATATGTTTGAAGTGAACAAGATGAATATTAACAATAATCTGATGACAGAGCT
 GAAACATACACATACACCTTAATCAAAAGCTTGGGGAATAATCTATTGGTTTGTGCTCTTCTGCTGCTG
 TGTATTGTGGGTGGAGATGGTTTCTTCTTCTTCACTTACGTTTGTGTTTATCTTTGATCTGAATACCTTTAA
 TTTATTTAAATCTGTGTTTGTGAGAGCTCTGCCATTTCTGAGTACCTGTTAGTTATTTATTTAGTGTATCGG
 GAGTGTGTTTAGTCTGTTTATTTGAGTAACACGATCTCCAAAGATTTCTCTTTGAAACGCTTTTTCCTCTC

FIGURE 143B

TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTGTTCCTTGACAATTTTGGTGCTCATGTGTTTTGGG
 GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAAGTTAAATTCACAGATCAAATGTGCCTTAATAAATTTGTT
 TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
 CCTGATGCTCATTGGAAAAATAAACCAAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
 ATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAAGTTAAACACGAAAAAA

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FIGURE 144

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRRAWLSVLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAAYRTWSKTI PGKVQFSSSEG
SDTSVPPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFWMRADDVYIKGDRLNENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPYGAEYILDLLLLYKHKHGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLVFNDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSPDNHFAFT
QKTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEDDVDFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCCGGCCTTGAGGTTCCACGCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCC**TATGA**AGCCCTTAGTCTTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
 CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAAACATGCTGTGTAATTC
 TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCATACATTAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTAT**TAA**ACAATAATATAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGA
 TTTAAGCAAACTGCATTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
 AAAAAATATTTCTATTGAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
 ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPVSPGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTFPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEFPYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGTCACTCTGTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACCCGTGTTCT
 CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGGGTTCTTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAACTGAGTTTGTGAAGGACTGCATTGCAGGGGGCGTGTCTCTCTAAGGC
 TAAAAACATCATCTCCCTCGGACATCGGCCTGTATGGGTGCTGTTCTAGTTCCTCAGATTTTAC
 GATGAGGAGGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCTCCACAG
 CCACAGCCAAGTGGAAGGTCCACAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTTGTGTTCCATCCACCTTGTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGGCGCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGTATGGGGATGATAATTGTTTTCTTCAAATCCAAGGGAAAAATCCA
 GGCGGAAGTGGACTGGAGAAAGAACGACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTCAC
 ATTTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCTTACACGATGAGGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAAGTCCCTTATTATACCC
 CTGCTGACATGTCAAGTTTGAAGGCTTGTGAGACCCCTATATCCAGCATGCGATGTATGACGA
 GGAAGGGGGACTCCCATATTATATGTCCAGTGTCTTGGGGAT**CG**AGACAGAGAAGACCCTG
 CTTAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGC
 GAGGTAGGATTTTCTCCTCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC
 TGAGGTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT
 TGGCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
 CATTAGGTTTGTGTTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGTCCTCATTTGCTAGTCACGGACAGTGATTCTTGCCTCACAGGTGAAGATTAAGAGAGA
 CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCAGAGTGTTCGTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACCTCTGTTTGGCTTATTCACATTAATTTACTTTTCTCTA
 TACCAATCACCCATGGAATAGTTATGAACACCTGCTTTGTGAGGCTCAAAGAATAAGAG
 GAGGTAGGATTTTCTCCTGATTCTATAAGCCCCAGCATTACCTGATACCAAAAACAGGCAAG
 AAAACAGAGAAGAGGAGGAAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTTCTAAATAAAATTTTAAACAATTAACTAAACAATATATTTAAAGATGATATATACTACT
 CAGTGTGGTTTGTCCCCAAATGCAGAGTTGGTTTAAATATTTAAATATCAACCAAGTGAATT
 CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

FIGURE 148

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLVSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFNRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQFSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTFPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**AATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAGAGCTTTGTTGGGAACCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAGAAGACCTACAA
 TTACTATAGCACATTGTCAATTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAATAATGCATTTTATAAA
 TCTCCATTAAAGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTTAAAGTA
 GATCCTCACTCAGTTAAAAATAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCACTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTGTGTGAGTGTCTCAGTGTGTTTACAACATATAA
 GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCCTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGTCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAAACAAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCT**TA**
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGATTTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTACGCAAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTACATTTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCTATTATGAAAAGGTCAAGCAAAGACAGCAGAATACCAATC
 ACTTCATCATTTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAAACAACACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAACTTCATGCAATGTACTTGTCTCAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

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FIGURE 150

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>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
>>subunit 1 of 1, 423 aa, 1 stop
>>MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVVRARRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYISTLSFTTD
KLYAEFGREASNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIFKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
MFKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPPVPTNAVHRVCLPDASYEFQPGDV
VTITGTGALKNDGYSQNHRLRQAQVTLIDATTCNPEQAYNDAITPRMLCAGSELGKTDACQDG
SGGPLVSSDARDIYWLAGIVSWGDECAKNKPGVYTRVTLALRDWITSKGTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
 CAGCCTGAGATCTTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATGC**TGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
 CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCTCAAGACTTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCCCTTGCCGGCTGTCCCTGCGACTACGACCACTGC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCTGCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCCACTACTGG
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCCTAGTGGCCGCTA
 ACGAGGCCGGGGCAAGCCGCGTGGCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
 CCTGCTTCGGGCCCTTGACGCCGCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC
 GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTC**TGA**
 AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
 GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTATAGTCCGGTACTT
 GGCGCTTTGTTTCTGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTTTAA
 AGCGCCAGATAATAATAATGTAACTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLWLDGSEA
AQKGPPNLATVRRaelKGLKPGGIYVVCVVAANEAGASRPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAAGVGTALALLSCAALVWHFCLDRWGCPRRAAARAAGAL
```

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC
 CCCAGCGCGACGATCGCTGCCGTTTGGCCCTTGGGAGTAGGATGTGGTGAAGGATGGGGC
 TTCTCCCTTACGGGGCTCAC**AATG**GCCAGAGAAGATTCGGTGAAGTGTCTGCGCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTTGACTTACTTTCTCTGTGTTTCTCATCCGGTCATGATTGCTGTTTGTGTTTCCCTATCAT
 TGTGGGAATGTTTAGGATTTGTGGAACGCTGAAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGCTTGTCTATTTTCTGTGTAGAAGTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACCTATGGTTCCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTCAGAGAGAGTTTAAGT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAATTTCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTGGAGAGGAACCAAACTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACAAATGATGTC
 CTTGAAGAATGACAACCTCTCAGCACCTGTCTGCTCCCTCAGTAGAAGCTTTGAAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTAT**TA**AAAGAAATGTACAGAAGAAAACCAAACTGTTTATTTGGAATTTGTGAATT
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTC
 CGCATCCATGCAAAACGAGTCACATATGGTGGGACTGGGCCATAGTAAAGGTTGATTACTT
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTTATTACTCAGCGATCTATTTCTTCTGATGCTAAATAAATATATATCAGAAAACCTTC
 AATATTGGTGACTACCTAAATGTGATTTTGTGCTGTTTACTAAATATCTTACCCTTAAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGATATATAAGTCTGTGTTAAA
 TCTGTATAAATTCAGTCGATTTTCAGTTCGTATAATGTTAAGAATAACCATTATGAAAGGAAA
 ATTTGTCTGTATAGCATCATATTTTTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAAACCACTAATTTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTCAGAAATGTAGTCTGGTCTTTAGGAAGTATTAAATA
 GAAAATTTGCACATACTTAGTTGATTAGAAAGGACTTGTATGCTGTTTTTCTCCCAATG
 AAGACTCTTTTGGACACTAAACACTTTTTTAAAGCTTATCTTGCCTTCTCCAACAAGAA
 GCAATAGTCTCCAAGTCAATATAAATCTACAGAAAATAGTGCTTTTTTCTCCAGAAAAT
 GCTTGTGAGATTCATTAACATGTGACAATTTAGAGATTCTTTGTTTTATTCTACTGATTA
 ATACTGTGGCAAATTTACACAGATTATAAATTTTTTACAAGAGTATAGTATATTTATT
 GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTCTCAGAAATATGGAA
 AGAAAATTAATGTGTCATAAATATTTTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRLCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIACCFLLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVWYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
 TGCACCTCGGGCCTCCTCCAGCCAGTGTCTGACCAGGACTTCTGACCTGTCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCAGAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG
 TGATTCTGGATAAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCACAGCAGGATCTGGA
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGGCCCTGTCT
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCTG
 GTGGTGGGTGGGAGGAGCCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACT
 GCTTCAGGAAACATACCGATGTGTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTCCCACTCACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGCTCAGTCCA
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCAACCGAGAAGA
 TGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC
 CTGATGTACCAATCTGACCACTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTGTAATGCTGCTGCCCCTTTGCACTGCTGGGAGCCGCTTCTTCTCTG
 CCCTGCCACCTGGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC
 CTCTGCCACAGCCTCAGCATTCTTGGAGCAGCAAGGGGCTCAATTCTGTAAAGAGACCC
 TCGCAGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGAGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACAGTTGTAATATAAAATGCAGTGCCTTACTGTGTGTATGACTACCGTT
 ACCTACTGTGTGCTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAA

FIGURE 156

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>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCCGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
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Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGAAAGCCTGGCATTCCAGAGGGAGGGAACGACGCGCATCCCAGGCTCCAG
 AGCTCCTCGGTGACAGTCTGTGGCTGAGCAATGGCCCTCCGAGCCCTGGGCGCTGGACCCCTGGAGCCCTCCTGGGCC
 TTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCCA
 GGTGCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACAGAGGGCCCTCAGGATTTTGACA
 CTCTGCTCCTGAGTGGTATGGAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCTTGGATATCCAGG
 ATCCAGGGGTCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCCTTTA
 AGAAGAAGAGCAATGAGACACAGTGTTCACACTCATCCGTGTCCTGGTTTCTTACAATGTACCCATCTCTACA
 CCTGGGCGACCTTCGCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCGG
 AGGACAAGGTCTAGGAGGAAAGGCCAAAGCCCTTTGACCCCGCTCACAGCATACGGCTGCTCTTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCGAGC
 CTGTCCTCAAGACCGACAACCTTCCTCGCTGGCTGCATCATGACGCTCCTTTGTGCGAGCCATCCCTTCGACCC
 AGGTGCTCTACTTCTTCTTCGAGGAGACGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGG
 CTAGAGTCTGCAAGAATGACGTGGCGGCGAAAGCTGCTGCAGAGAAGTGACACACCTTCTCTGAAGGCCAGC
 TGCTCTGCAACCCAGCGGGGCGAGCTGCCCTTCAACGTCATCCGCGACGCGGTCTGCTCCCGCGGATCTCCCA
 CAGTCTCCACATCTACGAGTCTTACCTCCAGTGGCAGGTTGGCGGGACAGGAGCTCTGCGGTTTGTGCCCT
 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAGAGTTGAACAAGAAACTTCAGCTGGACTA
 TCTATAGGGGCCCTGAGACCAACCCCGGCCAGGCGAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCT
 TCTATGAAGGACCACTTTCTGATGGATGAGCAAGTGGTGGGACGCCCTCTGCTGGAATCTGGCGTGGAGTATA
 CACGGCTTGAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCCACAG
 GGTGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGTCTCATCTGGTGAAGAGATTGAGCTGTTCCTGACC
 CTGAACCTGTTTCGAACCTGACGCTGGCCCCACCCAGGGTGACAGTGTGTTGAGGCTTCTCAGGAGGTGTCTGGA
 GGGTGCCCGAGCACTGTGAGTGTCTATGAGAGCTGTGTGAGCTGTCTGTCGCCGGGACCCCACTGTGCTCT
 GGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAATCATTA
 AAGAAGTCTGGCTGTCCCAACTCCATCTGGAGCTCCCTGCCCCACCTGTGAGCCTTGGCCTCTTATTAT
 GGAGTCATGGCCAGCAGCTCCAGAGGCTCTTCCACTGTCTACAATGGCTCCCTCTTGTCTGATAGTGACAGG
 ATGGAGTTGGGGGCTCTACACAGTGTGGGCACTGAGAATGGCTTTTCATACCTGTGATCTCTACTCTGGGTGG
 ACAGCCAGGACAGACCTTGGCCCTGGATCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA
 CCAGGTCAGTGGTGGGGCGCCCTGGCTGCCAGCAGTCTACTGGCCCCACTTTGTCTACTGTCACTGTCTCT
 TTGCCCTTAGTGCTTTCAGGAGCCCTCATCATCTCTGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG
 TTCAGGGCTGTGAGCACTGTGCGCCTGGGAGAAGGCCGCTTAAGCAGAGACCAACACTCTCAGTTCTGGCCATTCAGG
 AATGCAGGACCTCTGCCAGTGATGTGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAACACTCAGGCA
 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG
 CAGCACAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGATCACTGATGACACTCAGCAGGGGTG
 ATGCACAGCAGTCTGCCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC
 CCCCAGACCTGCTTACCATGATTAAGAAGCTGGAGAGGATCTCAGTTCTGGCCATTCAGGGAGCCCTC
 CAGAAACACAGTGTTCAGAGACCTTAAAAAAGCTGCCTGTCCAGGACCTTATGGTAATGAACACCAACATC
 TAAACAATCATATGCTAACATGCCACTCTGGAACATCCACTCTGAAGCTGCGCTTTGGACACCAACACTCCCT
 TCTCCAGGGTCTGACAGGATCTGCTCCCTCCTGCTTCCCTTACAGTCTGTCACCGCTGACTCCAGGAAGTC
 TTTCTGAAGCTGACCACTTCTTCTTCTGCTTGGGGGACACTGTGATCCCTCTGCGCTGGCAGCAATGC
 CAGGGGTAACTGAGCCTTCTTCACTCCTTTACCTAGCTGACCCCTTCACTCTTCCCTCTTCTTCTTGT
 TTTGGGATTCAAAAACTGCTTGTGACAGACTGTATTATTTTATTAAAAATATAAGGCTTAAAAAA

FIGURE 158

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVYGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDSFVAaipSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSrwTtYRGpET
NPRPGSCSVGPSSDKALTFMKDHFLLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLSHKAVVSGDSSAHLVEEIQLFDPPEFVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQIiKEVLAVPNSiLELPCPHLSALASYWShGPAaVPEASSTVYngSLLLiVQdGVGG
LYQCWATENGFSYPViSYWvDSQDQTLALDPELAGiPREHVkvPLTRVSGGAALAAQqSYWP
HFVTVTVLFALVLSGALiILVASPLRALRARGKVQGCETLRpGEKaPLsREQHLQSPKEcRT
SASDvDADnNCLGTEVA

```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AAGGTCCTTATAGCCGGGCGCAGGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
 TGAGC**ATGG**GCTGGGCGAGGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACACACAAAGAC
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGAATTTCTTTCTGGAAGAACTTTAGG
 TGGCAGAGGAAAAATTTGAAAACCTTATTAATGTTCTAGAATACTTTGGCGTTGCAGTCAGCTC
 ATTTTAAATAGAAAGGATATCATGGATTCTCTAAAGAATGAGAACTTCGACATGGTGATA
 GTTGAAACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGGC
 CATTTCTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACCAATCCCCCTTGTCTTATGTTCT
 CAGTATTCGGTTCTTGTCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG
 ATGTTCTTTAGTTTCTGCAGAGGGCAACAGCACATGCAGTCTACATTTGACAAACCATCAAA
 GGAACATTTACAGAAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCATTAATCTGACTTTGCTTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGTTTTAT
 GTTGAGGGCTTGATGGAAAAACCTATTAACACAGTACCACAAGACTTGGAGAATCTCATTGC
 CAAGTTTGGGGACTCTGGTTTTGTCTTTGTGACCTTTGGGCTCCATGGTGAACACCTGTCAGA
 ATCCGGAATCTTCAAGGAGATGAACAAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCAAGTGTCTCATTTGGCCCAAGATGTCCACCTGGGTGCAAAATGTGAAAATTTGTGGA
 CTGGCTTCTCAGAGTGACCTCCTGGCTCACCCAAAGCATCCGCTGTGTTGTCAACCCACGGCG
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCATTACAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCGAGTGGCTGCCAGTGTCTATCTGCGCTCCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA
 TGTCTTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGTGAAGGAGACAT**TAA**GGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
 TAATTTTGTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCTCT
 CTTGTCTCCTCTTGTTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCACTGACCTCAGATTTCAGCCTTAAATCCACCTTCTCTCATGCGCTCTGCCGAA
 TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATATCTTTCAGTTTCTGTTT
 TGTTCTCCACATATTTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAGGGC
 CGGACACAGGCTCACAGGTCTCCACATTTGGGTCCCTGTCTGTGGTCCCAAGTGAAGTCTCT
 TTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAGTTTACA
 GCGTTATCTCTCCCAACCTCACTAA

FIGURE 160

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGF
FMPDFKKEEKSYQVISWILAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAEWLF
INSDFAFDFAFRLPNTVYVVGGLMEKPIKFPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPISIRLFVTHGGQ
NSIMEAIIQHGVPMVGIPLFGDQFENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVFLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GGCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACATACCATTGTT
 CTCCATCCCCCAGGTCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGAGGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACGCCAGCCCTAGAGAGGGC
 AGACTATCAGGGTGCCCGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAAGAGGGGCAGA
 AGACCGGGGCATTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCCAAGCCACTGGC
 TACCAGGTCCTTACACAGTCCCGGGCTGCCCTTGGTTCCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTCAGAGCCCGTCTGCTGGAGGGGGAGTGCCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACAGGTCCTGGTGAACAGGGCGGTTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCCGTGTCCGGGGTGCTACAGCTTCCGGTTCCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCCTGTCTCTCAGCC
 TTTGCCAATGATCCTGACGTGACCGGGAGGCAGCCAGCCTCTGTGCTACTGCCCTTGA
 CCCTGGGACCGAGTGCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAATACT
 CAAGTTTCTCTGGCTTCTCATCTTCCCTCTCTGAGGAGCCCAAGTTTTCAAGCACAGAAT
 CCAGCCCTGACAACCTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCCTTCCACCCACCCACCCCAAGTTACC
 CTCCCAGCCACCTCTGCATCTGTTCTGTCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCATCTTTGCGGCCCTGCTCCTCCGGTTCCTCCACCCAGCTTCCT
 GGTCAATGCTGATCAGGACAGGTGGCGAGGTGAGCCTGACAGGCCCCACAGGAGCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGTGGCTGTTGAGGAAGGAAGGAGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCTTCTATGTCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGTCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAACATCGATAACCATGCATCCTCTGCTTGGCCACCTCTTGAACCTGCTCCAC
 CTTTGAAGTTTGAACCTTAGTCCCTCCACACTGTACTGTCTGCTCTCTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT
 CTGTGCTGTCTTATCTCCTCCTTAGGCTTCCTATTACCTGGGATTCCATGATTATCTCCT
 CAGACCCCTCTCTGCCAGTATGCTAAACCCCTCCTCTCTCTTCTTATCCCGCTGTCCCAT
 GGCCAGCCTGGATGAATCTATCAATAAAACAACTAGAGAAATGGTGGTCACTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAAATAATATCAAACTGTATACTAAATTAATAA

FIGURE 162

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEFVLLGECELVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLLIFPL

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Signal peptide:

amino acids 1-32

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FIGURE 163

[illegible]

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGGRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSGWRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGGCGGGATGGGGCCGGGGCGGGCGGGCGGCACTCGTGTAGGCCCCGACGACGAGGCCGGGCCGGGCCCA
 GGGCCGAGGAGCGCGGGCGGCAGAGCGGGGCGCGGAGGCGACGCCGGGACGCCGCGACGAGCAGGTGGCG
 GCGGCTGCAGGCTTGTCCAGCCGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGTGACCTTTGTGCTTTGGA
 CGGCTGTCTCAGCAGAGGGGCGGTGCACCCGCTCTGTAGCAGCGCCATGGGCGCTGCTGGCCCTCTCTGAAGACCCA
 GTTCGTGCTGCACCTGCTGGTGGCTTTGTCTTCGTGGTGGTGGTCTGGTTCATCAACTTCGTCCAGCTGTGCAC
 GCTGGCGCTCTGGCCGCTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCCGCTCGCTACTCACTCTGGAGCCA
 ACTGGTCATGCTGCTGGAGTGGTGGTCTGCACGGAGTGTACTCTGTTACGGACACGGCCACGGTAGAGCGCTT
 TGGGAAGGAGCAGCAGTCAATCATCTCAACCACAATTCGAGATCGACTTCTCTGTGGTGGGACCATGTGTGA
 GCGCTTCGGAGTGCTGGGGAGCTCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC
 GTGTAATTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGAGGAGGACCGGGACACCGTGGTCAAGGGCTGAG
 GCGCTGTGCGACTACCCCGAGTACATGTGGTTTCTCTGTACTGCGAGGGGACGCGCTTACGGAGACCAAGCA
 CCGCGTTAGCATGAGGTTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCCGGACCAAGGG
 CTTCAACACCGCAGTCAAGTGCTTCGGGGGACAGTCGACGCTGTCTATGATGTAAACCTGAATTCAGAGGAAA
 CAAGAACCCTCCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCCTCT
 GGAAGACATCCCGCTGGATGAAAAGGAGCAGCTCAGTGGCTTCATAAATGTACCAGGAGAAGGACGCGCTCCA
 GGAGATATATAATCAGAAGGGCATGTTTCAGGGGAGCAGTTTAAAGCTGCCCGGAGGCCGTGGACCTCCTGAA
 TCTCTGTGCTGGGCCACCATTTCTCTGCTCCCTCTTCAGTTTTGCTTGGGCGTCTTTGCCAGCGGATCACC
 TCTCCTGATCTGCTTCTGGGCTTTGTGGGAGCAGCTTCTCTTGGAGTTCGACAGATGATAGGAGAATCGCT
 TGAACCTGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCTAGGCAACAGAGCAAGACT
 CAGTCTCAAAAAAAAAAAAAAAAAACCCAGAAATTCGAGAGTTGAATGTGTAGTTACTGACATGAAAA
 ATTCAGTAGAGGTGAACAGCAGATTGAGCAGGCGAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
 TTTCAAGCTAATGAAAAAGAATGAAGGAAAAATTAACAGCTCAGAGCCCATGGTGCACCGTCACACAAATCAA
 CATATGCATGATGAGAGTCCCAGAAGAGAGGAGAGAAAGGTCAGAAAGAATGCCACAAGCTGATGAAAAACA
 GTAACCTACCCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTAT
 AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGACTTTTG
 ATCAGATTAAACAGCTATTCTCTCAGAAATCATGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
 AACCTTCAACTGTAAATTTGACATTTTGAATCTTGTAGTGGTCTGACCTGATCTTTGCTTCAGGACAGATTTTCA
 ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGACCTGTAGGAAGGCTGTCTTTAGGCCGGGCACAGTGGC
 TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTTGGGTCAGGCTGATCTCAAACTCCT
 GAGTTCAAGTGATCTGCCCGCTCAGCCTCCCAAAGTGTGTGATTGCAGGCGTGAGCCACTGCGCTGGCCGGA
 ATTTCTTTTAAAGCTCAATGATGGGGGCCAGGCACGATGGCTCAGCGCTGCTCCCAAGTACGCTTGGATTGTA
 AACATGCACCACCATGCTGCTAATTTTGTATTTTGTAGTAGAGCTGTTAGCCAGGCTGCTCTGCTCCTCT
 GACCTCAAGTGACCACCTGCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTGSCCTTGA
 GCATCTTGTGATGTGCTTATTGGCCATTGTATATCTTCTATCTCTTTGGGGAAATGTGCTTCAAGTCTTTG
 CCTTTTAAATTTTATTTATTTATTTATTTATTTTGTAGACAGGCTGTTGCTGTTGCCAGGCTGGAGTA
 CAGTGGCAGCTCTTGGCTCACTGCAGCCTCGACTCTGGGCTGCAGTGAATCTCCCACTGAGCTCCTCTGT
 AGCTGTATTTTGTATTTGTATTTGTAGCTGTAGTTTTGTATTTTTGTGGAGACAGCATTTTACCATGA
 TGCCAGGCTGGTCTTGAATCTCCTGAGCTCAAGTGAATGCTGCTGCTTCAAGCTCCCAAAGTGTGGGATTACAGA
 CATGAGCCAGTGCACCTGGCAAACTCCCAAAATTAACACACACACAAAAAACCACTGATTCAAAATGGGCA
 GAGGGCCGGCTGTGGCCCAATACAGGAGAGCTGAAGTGGGAGAGTCCCTTGGGATGAGAACTCGAGGCTG
 CAGTGAGTCAGGTTGTGCGACTGCATTCAGCCTGGACAACAGAGTGAGACCTGTCTC

FIGURE 166

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVG FVVSGLVIN FVQLCTLALWPVSKQLYRRLNCR LAYSLWSQLV
M LLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLLITFLGFVGAASFVRRLLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCTGGGGCA
 GCCACCAGGCATATTTCATCTTTGTGTGTGTTTTCTTTTGCCTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTGGTGGCAGGCAGGCCG
 GCTTACGCCCTGATACGGCCCTGGGTTAGAAGGGAAGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTTGTCTGCTTCCT**TAAT**GTGGTATGCCATGGGGTCTTTGCACAAGCCT
 TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC
 ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTTGTTTAAATGCTCTCATAAGACCACTTGTTCCTTTTGCAGCACTTGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
 TGCCTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCTACATGTGGTGGGTGCT
 CATGTTTTAGAGACTAAATGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
 GATGGTGTAGGGCCAGCATTGTAAATTACACAGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGTCTCTGATTCACTAGGCCCAGGTTGGGCATCTCTAACAAACTCCCACGTGATGCTGA
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
 TCACACCTATGATCCAGCACTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCACTGAGCCGAGATCAGGCCACTGTATTCCAACAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAA

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 1905-1920
 1921-1936
 1937-1952
 1953-1968
 1969-1984
 1985-2000

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHS LQCPGAATRH IHL CVCF SFALALGH FLLISLVGKGLSLSCGVGGRQAGLR LIRPWVRR
EGKINFY TNGDSWGLR PASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
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Important features of the protein:**Signal peptide:**

amino acids 1-28

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FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACT**ATGC**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTTAAATCTGTTTTTTTGTCTCTTGTAAGTACGCTTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCAAACCTGACCTTCACCTCTGGAACGAGAAGAGGTTTCTACCCAC
 ACCGTCCCTCGAAGCCGGGGACAGCCTCACCTTGTCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTA
 GCTGCGGCTTTCAAGGTGGGCCTTGCCTTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATT
 CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGTCTGTAGTCAATCACTGCCCTGGGG
 CCAGGACGGGCGGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
 CTAACCTTTTCATGTCTGTCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
 AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCACTTCTCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGAAGGAACCTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTCACTGAGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGCTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCATACCAG
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCTTCCCTC
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
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FIGURE 170

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FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCTCCTGCCCCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCTCTTCTCTGGGGAGCGGT
 GCCCCCATGGCGAGGCCGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGCGCTGGACCTGGGCACCTTACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
 GCCCCCGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGGAGACCTTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGAGGCATCTCGCCGTCCTCAGAGTCCTGTGGCGCGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAACGAACGCATCCGGCGG
 GACGTGAGGCTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
 C**TAG**GGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
 CCTGAGTTTTAAATTGAAAAATAAAGTGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

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FIGURE 172

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPVRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSRLRLTLEQPGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

[illegible]

FIGURE 174

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYKGPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDRG
VMAVTAVTATAASDRMESDSDSKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRPRRGPLGGRKKKKAPSADSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRREARRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTRRKSEGFMSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGEEAPQEKAEDKPSTDLAPVNGEATSQKGESAEDEKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDPRPGSDRQERERARGDSEALDEES

```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTCTCTCTGGATCTTCACCTTACCACTGCAGATCTTGGGACTCATCAGCCTCAATAATTTATATTAAATTA
 ACACCAATTTGAAGAAGCACTATGTTTTCATCTGAATGCTAATAAGATGAAAGACTTAAAGCCAGAAGCCAAAGA
 TTTTCACCTTTTTTCTGCTTTGATGATGCTAAGCACTGACCATCTTGTTTCTCCAGCTCACTGGCCATTTGAAGCA
 AAATATTCCAAGATCTCAAGCTACCACTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTGGGTTCTATC
 AGAAGGACTGGATTTCAACTCTCTCTCTTATAGATGAGGAAGAGGCAGGCTGCTCTTGGAGGCCAAGAACACAT
 CTCTTCTACTCAGCTGGTTGACTTAAACAAAAATTTAAGAGATTTATTGGCTGCTGTCGAAAGAACGGGTGGA
 ATTTATGAATTAGCTGGGAAGATGCCAATACAGAATGTGCAAAATTTATCAGAGTACTTCAGCCCTATACAA
 AACTCACATATATGTGTGGAACTGGAGCATTTATCCCAATATGTGGGTATATTGATCTTGGAGTCTACAGAAG
 GGATATTATTTCAAACTAGACACACATAATTGGAGTCTGGCAGACTGAATGTCTTTTGATCTCTCAGAGCC
 TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTCTGGCAAGATACTGCAT
 CACTCGATCCCTTGGGCTACTCATGACCACCACTACATCAGAACTGACATTTACAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATTGGAACCTTCTCATACACAGACACCTACAATCCAGATGATGATAAAATATATTCTCTTTTCG
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTTTCTCGAGTTGGAAGAGTTTGAAGAATGATGT
 AGGAGGACAACGCAGCCTGATAAACAAGTGGACGACTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
 TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGTCTTTACTACAAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCACTGGCTGACAT
 CAGAGCAAGTTTTAATGGTCCATATGCTATAAGGAAAGTGCAGACCATCGTTGGGTGCATATGATGGGAAT
 TCCTTATCCACGGGCTTGCTACATGTCCAAGCAAAACCTATGACCACTGATTAAAGTCCACCCGAGATTTTCCAGA
 TGATGTCACTCAGTTTCTAAGAGCGGCACTCTGTGATGTATAAGCCGATACCCGTTTCAGGAGGACCAACGTT
 CAGAGAACAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAGAGATGGCCAGTACGA
 TGTATGTTTCTTGGAAAGACATTTGGAACCTGTCTCAAAGTTGTGCAGCACTTTCAAAGGAAAGTGGAAATATGGA
 AGAGGTAGTGTGGAGGAGTCCGAGATTTAAGCACTCATCAATCATCTGAACTGGAATGTCTCTGGAAGCA
 GCAACAATTTGACATTTGGTCCGAGATGGATAGTTTACGCTCTCTTGCACAGATGCCCACTTATGGGAAAGC
 TTGCGCAGACTGTGCTCTGCCAGAGACCCCTACTGTGCTGGGATGGAATGACTGCTCTGATATGCTCTAC
 TTTCAAAGAGGAGCTAGACGCCAGATGTAAATATGGCGACCCTCAATCCCAAGCTCTGGGACATCGAAGACAG
 CATTAGTCATGAACTGCTGATGAAAGGTGATTTTGGCATTTGAATTTAATCACTCAACCTTTCTGGAATGTATACC
 TAAATCCCAACAGCACTATTAATGGTATATCCAGAGGTTCAGGGAGTGAAGTATCGAAGGATTTGAAGCCACA
 TGAAGAATCAITCAAACGAAATATGGCTACTGATTCSAAGTTTGCAGAAGAAGATTTCTGGATGTATTACTG
 CAAAGCCCAGGAGCACACTTTATCCACCACTAGTGAAGCTGACTTTGAATGTCAATGAGATGAACAGATGGA
 AATATCCAGAGGGCAGAGCATGAGGAGGGGCGAGTCAAGGATCTATTGGCTGAGTCAAGCTTGAATACAAAGA
 CTACATCCAAATCTTAGCAGCCCAAACTTCAGCCTCGACCACTGCTGCGACAGATGTGGCAACAGGACAAGCG
 GAGACAGAGAAACAAGGGGGGCCAAAGTGGAAAGCACATGCAAGGAAATGAAGAAAGAAAGAAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACCTAGTTTTCTACTTAATTTAAGAAAGAAATTCCTTACC
 TATAAAAAACATTCCTGTTTGTATATCCCTTATAGTAATTCATAAATGCTCCCATGGAGTTTGTGCTAAGG
 CACAAGACATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAATTCATTTGAACAGTTT
 CCAAGAACAAATCTTGACAAGCAAAAGTATAAGAAATATCTCAAATATAGAGGGTTTACAGTTGTAATGTGTTT
 TGTTTGTAGTTTGGAAATTTATTGTCATGTAAATAGTTGAGCTAAGCAAGCCCGAATTTGATAGTGTATAGGT
 GCTTTATTCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGACAGATATAT
 CATTTCTTATGAGAACAGCTACCTTGTGGTAGGGAATAAGAGGTGACACACAAATTAAGACAACCTCCCATATC
 AACAGAACTTTCTCAGTGAGCAATCACTCCTGGAGAAATGGTATAGGAATTTGGAGAGGTGCATTTATTTCTT
 TGGCCACTGGGGTTAAATTTAGTGTAACAACATTTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT
 ATTCAGTACTGAGGATCAACAGGTTACAGAGAGAAGTTGGTGTAGTTATGTTTGTGTTTATAGAGTATATCTA
 GCTCTACAGGACAGATGCTTAATAAATACTTTAATAAGATATGGGAAATATTTTAATAAAACAAGGAAACA
 TAATGATGTATATGTCATCCTGATGGGAAGCATGCAGATGGGATTTGTAGAAGCAGAGAAGGAAGACAGCCAT
 AAATTTCTGGCTTTGGGGAACATCATATCCCATGAAAGGAGAGAACAATCACAATAAAGTGAGAGTATATGAA
 TGGAGCTCTTTTCACTAGGTATATAGTACCTGCCAATTTGTAATTCATCTGTAAAAAATCTAGATATAACA
 AACTGTATGCAAAATCTGAGGAACACATAAATCTCTCTGAAGAATCATAGGAAGAGTAGACATTTTATATAAC
 AATGATTTTCAGTATATATTTCTCTCTTTAAAAAATATTTATCATATCTGTATATATTTCTTTTATCTGC
 CTATTATCTCTCTGTATATGGAATTTGTGATATATTTGAGTGAATAGGAGAAACAATATATATACACAGAGA
 GTTATTAAGAAATGACATTTCTGGGAGTGGGATATATATTTGTGAATACAGACAGTGTAAATTTTAAAC
 AACGGAAAGGGTAAATTAACCTTTGACATCTTCACTCAACCTTTCTCATTTGCTGAGTTAATCTGTTGTAAT
 GTAGTATTGTTTTGTAAITTAACATAAATAAGCCTGCTACATGT

FIGURE 176

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPIRLKLTYKDLLSNSCIPFL
GSSEGLDFQTLTLLDEERGRLLLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDI SEHYWLNAGKFIGTFF
IPDTYNPDDDKIYFFFRESEQEGSTSDKTI LSRVGRVCKNDVGGQRS LINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVVLEE
LQIFKHSSIIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYKACADCCCLARDPYCAWDGNA
CSRYAPTSKRARRRQDVKYGDPITQCWDIEDSISHETADEKVI FGI EFNSTFLECIPKSSQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTNLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQLSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRHHRDLDELPRAVAT

```

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACCAGCGGGGAGCAGA
 CAACTCCACAGTAAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGATATTTCCGCCACCCCAAG
 CTCAGCAGTTTACGCCAGCAGGGGACTGATCAGGTGTGTGTCCTGGAGTGGGAGGAGCAAGGCGTGGCTGGCAAGA
 CTCGGCTCGGAAAGAGGTTTACAGCGCTTACCAAGCCAGGATCGCCGTGACTACAAGATCGAGAAACCATGGCATC
 GGGTGAGTGGGGGGGACAGGTGTGTCATGTGCACCTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGCTGAATCCTTGG
 AGCCATTTAGGGTGTGATGGAGTACAGAGGGGAGGGAAAGGTATTTAAGGTAAACGATGTGGGCACAATAGTTAA
 GAGCAGAGTTTGGAGCTAGACGCACATAGGTTCAAAATTCCTTCTGTGTGCTTCCATGTTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACTCTCTGACTTCAATTTCCCTATCACTAAAGTAGGGCCAAATAATGACACCCACCTCAT
 AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAAGTACCAGTCCCATAGTAAGTCTATGCCCCACAG
 TATTTCCACCCACCCCTGTTCTCTGCTTCCCAACACAGGTACTGCAACGACTGGAGCAGAGGGCGGACAGGCTT
 CAGAGCGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGCCACAGGTGAGCC
 AGGTGAAGGGGGCTGCCGGCTGGCCCTGCTCAGGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCAGGATGAGTGGAGCAGGAGCGCGGCTCAGTGAGGCTCGGCTGTCCACAGAGGGAACCTCTCTC
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
 CCCAAGCCTGGCCACGAGGGGCCCTCCCTGCCCTGCACACGTGTTATTTGCTATCAGGACGGGCTGAGGATG
 AGCTGACAATCAGGAGGGTGAAGTGGCTGGAGGTATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA
 ACCAGCAGCGGAGGTTAGGCTTTCTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCACAGAGAGCAGCC
 AAGCAGTAGCAATTCCTCGGGGCGAGAGCCACAGCATTTCTGGCAGAGCCGCTGTACAGTACACCCAGACAGA
 GTGACAGGAGCTGAGCTTCCCTGAGGGGCACTCATCGTCTGCTGCCGGGGCCAGATGGATAGATGAGTGACG
 GCTTTGAGGGGAGAAATTTGGGGCCGTGTGGGGTCTTCCCTCCCTGCTGGTGGGAAGAGCTTCTGGGCCCC
 CAGGGCCGCTGAATCTCTGACCTTGAACCTGAACAGATGCTGCCGTGAGCTTCTCTCTCCAGCTTCTCCCACTGAC
 CTACTCTGTGTGGATGGGCCCTTGCACCTGTCTGCCCTGGGAGCAAGCGCTGGACTTCCCTGGGTCTCTGG
 AACTAGTACCACTCAGCTCAGGCCGATGCTCAACACCTCCCGCCGGCTAAAGCCCGGATCCTGGCCAC
 CAGATCCCTCACCTGAAGGCCAGGGAAGCCTTGACCCCACTGATGCTGCTGTCTCTATCTCAAGCTGTGAGA
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAGCTGGAATGCCCTTATTTTCCACCTCACTCTCAAGGGT
 GGAATTTGCCCTTCCATTTCTAGAGCTGGAACCCACTCCTTTTTCCTATCTCTATCACTCTTAGGACC
 GGAACCTACTACTTCTCTCTGTCATGACCTTATCTAGGGTGGTGAATGCTGGAATCTCTGGGCTGGAAGCC
 ATCCATCAAGSTCTCTAGTAGTCTTGGGCCACCTCTTTCCACCCCTGGCTCATGACCCACCCACTCTGGATG
 CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAAGCCAGGATCGGAAGCAG
 CTGTAATGCTCTGAGCGGATTTATTGACAATGAATAAAGGGCAAGGAGCCAGGCCAGGGCTGGGCTCTTTGTG
 CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACCAACGGGACAGGGGCTGCTCCAGCTGCCAC
 GCTCTATCATATGGAGCAGGTGTGGGGAGGCGGGGAGGAGCCTGTTGCAGGACGGGGAGGAGGAAGAGAC
 TGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGCTCCTC
 AGCTGGGGGCGAGTGTCTCCAGTGGAGGGGAGGGCTTTCAGGCCACCCACCCCTGGCCCTGCGAGCTGGTAG
 TCCATCAGCAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTCTTCAAGCTGTGTCCAGC
 TTTTCCCTGGGGCTCCAGGACCTTCCCTACTCCACCAACCAAGGGATTATAGCAAAAGGTTAGGCTGCG
 AGTTTACTCTGGGGTTAGGGAGCCGAAGGCTTAATAGTTAAGTAGGTGATGGGAAGATGAGATTACTCTACA
 TTTAGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCTGTGGTAGAGACACTGAGAGAAGGGGAGGGG
 TCAACAATGAGAGACCAGGATAGGTCTTATCAGTGCCTCCAGAGTAGAGAGCAATAAGAGCCAGCCAGCTGCG
 AGTCCCGCTGTGTTTTCTACTCTGGTGATCAGAAGTGTCTGGTTTGGCTGGCCATTGGCTCTTGAAGTGG
 CAGAGCCTGGGCTTGGGCCCTTCCCTCCGGCCCTCAGTGTGGCTCTGCAGAGACTCTGGGGTTCCCTTCAAGTG
 CAGAGGGGTTAGGCTGTCTTCCCTGAGTCTTCCACTGTACTGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
 TCTCAGGGGCGACCTCTCCATGGCAGGCATCCCTGCTTGGGCTGCCCTCCCCAGACCCCTGACACCCCTG
 GGTCTGTCCCCACAGAGCCCACTCCTGTCTGTGGGGAGGCCATCAGGCTGTGTGTCAGTCCATAGGCTG
 TCTCAATGTGTACCCGGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACTCAGAGGCTGCTTG
 GCCCTCCCTCTGACAGGGACCTCTGAGTTTGGTGGCTACTTCCCTGCGGCTAAGGTAGGGGAGGCTTCTC
 AGATTGTGGGACACATTTGTGTAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGGCCAGGCCACTT
 TTGGGATCAGTGCCTGATCACTGGGCCCTTACCTCAGCCCTCTTCCCTGGAGCACTGTGATGTGGAGGGGCTC
 CAGAGAACACAGTGGTCTCCCTGTCCGGGGGCGGCTTTTCCCTCTCTGGAGCGTCCCTGACGGACAGGTGAG
 GCTCTTCTGCTGGGCTGCAATGATGATCAAGGGGCTGCAGAGCCAGTGCATGTGATGTGGAGGGGCTC
 CGTCTGCTCAGGCTGGAGTGGCACTCCACTGGACAGCAGGAGGAGGGAGTGAGGCTAACATTTCCATTTCCCT
 TCTATGTTTGTCTTCTTACGTTCTCTCAGCATGCTCTTAAACCCCGAGAAGCCCCAATTTCCCGAGGCCCATTT
 TTTCTTGTCTTTATCTAATAAATCAATATTAAAG

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></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTVLCLFNQVLQRLQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAAARLALLQGAGLDVERWLKPMATQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELTTITEGWLEVIEEGDADEW
VKARNQGEHGVGFVPERYLNFPLDSLPESSQDSDNPGCAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGDDGFWRGEFGGRGVFSPSLLEVLLGPPGPPELSDPEQMLPSPSPPS
FSPAPTSVLQDGAPVLPDGDALDEPGFLDMMAPRLRPMRPPPPPPAKAPDGPGHDPDLT
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[illegible]

FIGURE 179B

ATGTGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTTGCCAATAATAATACCTCCCTTAGAAG
 TTTGTTGTGAGGATTAATAATGTAATAAAGAAGCTAGCATACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAGGAAA

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FIGURE 180

>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

>>subunit 1 of 1, 837 aa, 1 stop

>>MW: 90167, pI: 8.39, NX(S/T): 1

MSQ¹GS²HP³GR⁴GL⁵AG⁶R⁷WL⁸GA⁹Q¹⁰PC¹¹LL¹²PI¹³V¹⁴PL¹⁵SW¹⁶L¹⁷V¹⁸W¹⁹LLLL²⁰LL²¹AS²²LL²³PS²⁴AR²⁵LA²⁶S²⁷PL²⁸PRE²⁹EE³⁰IV³¹
 F³²PE³³KL³⁴NG³⁵SV³⁶LP³⁷GS³⁸GA³⁹PAR⁴⁰LL⁴¹C⁴²RL⁴³Q⁴⁴AF⁴⁵GE⁴⁶T⁴⁷LL⁴⁸LE⁴⁹EQ⁵⁰DS⁵¹GV⁵²QE⁵³GL⁵⁴TV⁵⁵Q⁵⁶Y⁵⁷LG⁵⁸QA⁵⁹PE⁶⁰LL⁶¹GG⁶²AE⁶³P⁶⁴
 GT⁶⁵Y⁶⁶LT⁶⁷GT⁶⁸ING⁶⁹DP⁷⁰ES⁷¹VAS⁷²LH⁷³WD⁷⁴GG⁷⁵ALL⁷⁶GV⁷⁷LQ⁷⁸YR⁷⁹GA⁸⁰EL⁸¹HL⁸²Q⁸³PLE⁸⁴GG⁸⁵T⁸⁶PN⁸⁷S⁸⁸AG⁸⁹GP⁹⁰GA⁹¹HL⁹²RR⁹³KS⁹⁴P⁹⁵
 AS⁹⁶G⁹⁷QG⁹⁸PMC⁹⁹NV¹⁰⁰KAP¹⁰¹LG¹⁰²SP¹⁰³SP¹⁰⁴RR¹⁰⁵PR¹⁰⁶AK¹⁰⁷R¹⁰⁸FAS¹⁰⁹LS¹¹⁰RF¹¹¹VET¹¹²LV¹¹³VAD¹¹⁴DK¹¹⁵MA¹¹⁶AF¹¹⁷HG¹¹⁸AG¹¹⁹LK¹²⁰RY¹²¹LL¹²²TV¹²³MA¹²⁴AA¹²⁵
 AA¹²⁶KA¹²⁷FK¹²⁸HP¹²⁹SIR¹³⁰NP¹³¹VS¹³²LV¹³³VT¹³⁴RL¹³⁵VIL¹³⁶GS¹³⁷GEE¹³⁸GP¹³⁹QV¹⁴⁰GP¹⁴¹SA¹⁴²AA¹⁴³Q¹⁴⁴T¹⁴⁵LR¹⁴⁶SF¹⁴⁷CA¹⁴⁸WQ¹⁴⁹RGL¹⁵⁰NT¹⁵¹PED¹⁵²SG¹⁵³PD¹⁵⁴H¹⁵⁵F¹⁵⁶
 DT¹⁵⁷AIL¹⁵⁸ET¹⁵⁹RQ¹⁶⁰DL¹⁶¹CG¹⁶²VST¹⁶³CD¹⁶⁴TL¹⁶⁵GM¹⁶⁶AD¹⁶⁷VG¹⁶⁸TV¹⁶⁹CD¹⁷⁰PAR¹⁷¹SCA¹⁷²IVED¹⁷³DGL¹⁷⁴QSA¹⁷⁵FTAA¹⁷⁶HEL¹⁷⁷GH¹⁷⁸VFN¹⁷⁹ML¹⁸⁰HD¹⁸¹
 NS¹⁸²KPC¹⁸³IS¹⁸⁴LN¹⁸⁵GP¹⁸⁶LST¹⁸⁷SR¹⁸⁸HV¹⁸⁹MA¹⁹⁰PM¹⁹¹AHV¹⁹²DP¹⁹³EEP¹⁹⁴W¹⁹⁵SP¹⁹⁶CS¹⁹⁷AR¹⁹⁸FI¹⁹⁹T²⁰⁰DF²⁰¹LD²⁰²NG²⁰³YGH²⁰⁴CL²⁰⁵LD²⁰⁶KPE²⁰⁷AP²⁰⁸LHL²⁰⁹
 PV²¹⁰TF²¹¹PG²¹²KDY²¹³DADR²¹⁴QC²¹⁵QL²¹⁶T²¹⁷FG²¹⁸PD²¹⁹SR²²⁰HCP²²¹QL²²²PP²²³CA²²⁴AL²²⁵WC²²⁶SG²²⁷HL²²⁸NG²²⁹HAM²³⁰CQ²³¹TK²³²HS²³³PW²³⁴AD²³⁵GT²³⁶PC²³⁷G²³⁸
 PA²³⁹QAC²⁴⁰MGG²⁴¹RCL²⁴²HMD²⁴³QL²⁴⁴QDF²⁴⁵NI²⁴⁶PQ²⁴⁷AG²⁴⁸GW²⁴⁹GP²⁵⁰WGP²⁵¹WGD²⁵²CS²⁵³RT²⁵⁴CG²⁵⁵GG²⁵⁶VQ²⁵⁷FS²⁵⁸SR²⁵⁹DC²⁶⁰TR²⁶¹PV²⁶²PR²⁶³NG²⁶⁴GKY²⁶⁵
 CE²⁶⁶GR²⁶⁷TR²⁶⁸FR²⁶⁹SC²⁷⁰NTE²⁷¹DC²⁷²PT²⁷³GS²⁷⁴ALT²⁷⁵FR²⁷⁶EE²⁷⁷QCA²⁷⁸AY²⁷⁹NH²⁸⁰RT²⁸¹DL²⁸²FS²⁸³F²⁸⁴PG²⁸⁵MD²⁸⁶WV²⁸⁷PR²⁸⁸YTG²⁸⁹VAP²⁹⁰QD²⁹¹CK²⁹²
 LT²⁹³CQ²⁹⁴AR²⁹⁵AL²⁹⁶GY²⁹⁷YV²⁹⁸LE²⁹⁹PR³⁰⁰VD³⁰¹GT³⁰²PC³⁰³SP³⁰⁴PD³⁰⁵SS³⁰⁶VC³⁰⁷VQ³⁰⁸GR³⁰⁹CI³¹⁰HAG³¹¹CD³¹²RI³¹³IG³¹⁴SK³¹⁵KK³¹⁶FD³¹⁷KCM³¹⁸VCG³¹⁹GD³²⁰G³²¹
 SG³²²CS³²³KQ³²⁴SG³²⁵SFR³²⁶KFR³²⁷YGY³²⁸NN³²⁹VV³³⁰TI³³¹PAG³³²ATH³³³IL³³⁴VR³³⁵QGN³³⁶PG³³⁷HRS³³⁸IY³³⁹LAL³⁴⁰KLP³⁴¹DG³⁴²SY³⁴³AL³⁴⁴NGE³⁴⁵YTL³⁴⁶
 MP³⁴⁷SP³⁴⁸TD³⁴⁹VVL³⁵⁰PGA³⁵¹VS³⁵²LR³⁵³YG³⁵⁴ATA³⁵⁵SET³⁵⁶LS³⁵⁷GH³⁵⁸GLA³⁵⁹QPL³⁶⁰TL³⁶¹LQ³⁶²VL³⁶³VAG³⁶⁴NP³⁶⁵QD³⁶⁶TL³⁶⁷RY³⁶⁸SFF³⁶⁹VPR³⁷⁰PT³⁷¹
 PST³⁷²PR³⁷³PT³⁷⁴QD³⁷⁵WL³⁷⁶HRR³⁷⁷AQ³⁷⁸ILE³⁷⁹IL³⁸⁰RR³⁸¹RP³⁸²WAG³⁸³RK³⁸⁴

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT
 AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGATTACATGGAAATTGATCCTGTG
 ACCAGAACTGAAATATTAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
 TTAAAGTGATTTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTGGGTCCCAGCAGAAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATTCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCCGTCACGCCAGACAGCAAGTGAGGAAGAACCTCCAATAAATGACTATACTG
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTGCTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC
 GCATGCTGGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCAGAAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

FIGURE 182

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>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
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Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACC**ATG**GCCAGCAGCGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGCCATCCTCGGCGGCACCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
 CTCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCCCTGCTTTGCCTGTCTGCCAGGACGAGGCACCTACAGGCCCTACCAGGCCCGGCC
 CAGGGCCACCACGACCACTGCAAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGCTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATATATATAT
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGC GGATGTGGCTGTTTATGAAAAAAAAAAAAA

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FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLITTLPHWRRTAHVGTNILTAVSYLKGLWMCECVWHSTGIY
 QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTFAKTTFAILGGTL
 FILAGLLCMVAVSWTTNDVVQNFYNPLLPSPGMKFEIGQALYLGFISSSLSIGGTLCLSCQ
 DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

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FIGURE 185

GAGCTCCCCTCAGGAGCGCTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGCGCGCAGGGCGGGCGGCCAGGATC**ATGT**CCACCACCACATGCCAAGTGGTGGCGTTCTCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGTCTGGAGGAGCTGC
 GTGAGGCAGAGTT**CAGGCTT**CACCGAATGCAGGCCCTATTTACCATCTCTGGGACTTCCAGC
 CATGCTGCAGGCAGTGCAGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTCTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGCCAAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTT**CAGACCAGGTACACATT**TTGGTGC GGCTCTGTTCGTG
 GGCTGGGTGCGTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
 CCTGGCACCAAGAAACCACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCAGCTGGCTTTGGGTCCAACACCAAAACAAGAAG
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAAGCACGACTA
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
 AACAAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTTCTCTCCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCAAGAAAACCTTTTGAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAGTTTACCAAAACCAAGTCATTTTCAGTTTGGAGCAACCAACCTTTCTACTG
 CTGTTGACATCTTCTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
 TCTCTTTCTGTGCGGGTCAGAAATTGTCCTTAGATGAATGAGAAAATTATTTTTTTTAAAT
 TTAAGTCCCTAATAATAGTTAAATAAATAATGTTTGTAGTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTTGCTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCCTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCTTAGGAAGTAGGTTAA
 ACTAATCTTTAA

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
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Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTCCG
 GAGTCCAGCTGGCTAAAACTCATCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAAATGGTGGGCACAGTGGCTGTCACTGTCAATGCCTCAGTGG
 AGAGTGTGCGCCTTCATTGAAACAACATCGTGGTTTTTGAAACTTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGG
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTT
 TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAAGGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTAACTTTACTATAAAGC
 CATGCAAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTTTCAGCAGAATGAGATATTAACCCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT
 AAAGACTGCATATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTGTG
 AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAAATGCTCCTCATTATATAATGA
 AGATTAAATGAAGGCTTTAATCAGCATTGTAAGGAAATGAATGGCTTCTGATATGCTG
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCTCTCTCTCCAGAGGCTTTTTTT
 TTCTGTGTATTAAATTAACATTTTTAAAACGCAGATATTTTGTCAGGGGCTTTGCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAATATTTTTGTTTTGTATTGGAAGAAGATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATTTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACA
 ACAAAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATG
 TCATTTTTGTCTGTGAAAAATAAATTTCTTCTTGTACCATTTCTGTTTAGTTTTACTAAA
 ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGA
 AAGTTGTGTGCGAGCTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
 TTAATAAATGTACATTTTTCTAATT

FIGURE 188

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
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Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**ATG**CCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
 CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTCGCTGGTGCAGAGCACCGGCC
 AGATGCAGTGCAGGTGTACGACTCACGTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTGGCTTGTGGTCTACCTTGTGGGGC
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTACCTCTGGGA
 TTGTCTTTGTCTATCTCAGGGGTCTTGACGCTAATCCCCGTGTGTGGACGGCGCATGCCATC
 ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGGCTCCCT
 CTA CTGGGCTGGGCGGCCTCAGGCCTTTTGTGTGGGTGGGGGGTTGTCTGTCTGCACTT
 GCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCTT
 GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**TGAC**GTGGAGGGGAATG
 GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGCGAGTGCCCAACAGCTTTGGGATGGGTT
 CGTACCTTTTGTTTCTGCCTCCTGCTATTTTCTTTTACTGAGGATATTTAAATTCATTT
 GAAAAC TGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG
 ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
 CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGTGTGCTGGCTTTGCAACAAGACAGAC
 TGTCCCCAAGAGTTCTGTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
 CCCCCATCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGTCTGATAAGACG
 TCCACCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
 CTTCTGCCTGCCCCCTCGTCTCACCCCTTTACTACTCACATTTTATCAAATAAAGCATG
 TTTGTAGTGCA

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FIGURE 190

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Transmembrane domains:

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FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACTCCGAATTGAACCACTCTTCAAAGTAAAGGCAATGGCATTCTATCCC
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTGGCATGGTGGGACTCTTGCCACAACCCCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGCTCCTTGTGGCTCTCCC GCCCTGGAAACAGCCCGGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCCCTCTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTTACA
 ACCCAGCCATCCACATAGGTGAGAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
 AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTTATAAAGTCTGTAGAACTGTAAGTATGTGAGGCAGGA
 GAACCTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTACTGTTGGTAGG
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAA
 GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

FIGURE 192

```
>>/usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA73737
>>subunit 1 of 1, 173 aa, 1 stop
>>MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRVLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFIILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMSKTSYSY
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Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATGA**AGATCACTGGGGGT
 CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
 AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
 CATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCAC TTGTGTACC
 GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA
 TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
 AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG
 ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
 TTTTTTTTAAACACGTCAATAAAAAAATAATCTCCGAGA

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FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVFCSSEASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

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FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCCTCGCCCTCCTGCTCGCGCCC
 CGCCGCC**ATGG**GCTGCCTCCCCGCGCGGCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGC
 TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA
 AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGCCCGTTGATGAGAATAAAGCCAAAGA
 ATTCCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCAGGTGC
 AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
 ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
 CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
 TCAACTACGATGACTAC**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTTC
 TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTCAGCAGAT
 CTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAAACAACACATGTAAATGCCTTT
 TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

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FIGURE 196

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><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

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FIGURE 197

CGGCTCGAGCCCGCCGGAAGTCCCCAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
 GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
 CGTCCITTTTCTCGGTGCTTGCTTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
 CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCAAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
 CCCCAGACTCCCCGAGGAGCCCCCTCGTGCTACGGCTGAAATTCCTCAATGATTACAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
 GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAAATCCCCCTGCCCCGCGGGTCCGAGCCCCGCCCTCCGGGCTGGAAATCGGCAGCCT
 GCTGCTGCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
 CCTTCTTTCCCTGACCGCCACTCTGGGCCCTGGCCGGCTTACCCCTGCTCCTCAGTCTCCTG
 GCCTTTGCCATGTACCGCCCCTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC
 GGACCTTGCTCCCCGCGCCGCGGGGAGCTGCTGCCTGCCAGGCCCGCTCTCCGGCCTG
 CCTCTTCCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGCGCGGAGG
 CCCC GCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCGCA
 CTGGGAGTGGGCTCCTCGGGTGGGCATCTGCTGTGCTGCCTCGGCCCGGGCAGAGCCG
 GGCCGCCCGGGGGCCCTCTTAGTGTCTGCGCGAGGACCCAGCGCCTCCAATCCCTGAC
 AGCTCCTTGGGCTGAGTTGGGGACGCCAGTCTGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
 GGGCAGAGGAGTTCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAA
 AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
 RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT
 IGSLKRTQFFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
 EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFFFLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

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GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGCTGCAAGACCCTAAGAACCATCAGCCC
TCAGTGCACCTCTCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GGAGACTTTGGATTGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAGATTAATGAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCAGATCAACAGCCACTACTGGTGAACGATTATAAGAGTTACTCGGAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCAGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGCAACAGGGTGCGGGTGCACCGTGG
AGTCATTTCAAGACTCCTGCCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
CTTCATGTTATTTCTTCTCTCCATTCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTCTTGCTGGCTCTCCTTACTCCCATCTGACCAACAGCTCCGCTGGTTCCTGTCTGTTAT
TTGTAACCTGAGGACCACAATAAGAAATCTTTATATTTATCG

FIGURE 200

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><subunit 1 of 1, 148 aa, 1 stop
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><MW: 16896, pI: 6.05, NX(S/T): 1
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MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCHVDCQDLLNPNLLAGIHCARIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
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Signal peptide:

amino acids 1-18

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FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTGACGCCCTGCTTGACTGAGAAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATTTATTTTTTCCCAAGGAGAAAAACCGGGTAAAGGGAGGGAAGCAATTC
 AATTGTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTTGGGTGAAACTTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGCTCTGCACACGC
 TGTTGGCAAAATGTCAGGACAGGTTAAGTGACTGGCAGAAAAACTTCCAGGTGGAACAAGCA
 ACCCATGCTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAAGCTTGAACATGAC
 CTGTTGCTATTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCTCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACCACACCTGCAACAGACTGTACAGCCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCCTTACCCAGGGCCAGAAGGAACAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGAGGTTGCTGAAGAAGAGGAGTTGACCCCGTTTACGCTGGACCCAC
 GTGGCCTCCAGGAGGCTCAGTGCCCGCATCCCTCCAGAGGGCTCTGCCCGAGGTGCGG
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCCAAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCCCTGGTCCACTCTCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTTCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
 CTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCCACTGCGAGTGGCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATTGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGAGCTGACGCGTGGGTGTTGGACTGGAAGCTGGATTCCACTGGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAGGCCCATCAGGAGGCCCTGTG
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTGCGTGGCAGGTGGTGAAAACCTCGAAGTGTCTTTCAAGGCTTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT
 TCCCCCTTGACCAGGAGGCCACCTGAGGAACAGGGTTCGCAATTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTCAAGCATAGCCCAGAGGCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAGGAGACTGGGTGTGTCGGACATTCCACTGG
 TTTCTGGCTAATGTCTACCTGAGCTGTACCATCTGAACCCAGGCCAGTTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGACATCCTGGGCT
 GTCCTCATGGTGTGGCTCCTTGCACTGACAGCCGGCAGCAACAGTACTGCAACACACAGC
 AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTGAGGCAGGAGCAGGT
 GATTCCTCAGAAGTGCAGGAGGAAGGCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCACATTTCTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAC
 AATAAAGATTGTACCTGCGTCCGTGTGATGGAAGAGCCCGCAGCAGGTGGCGATTGACCA
 GATAAATGCTGTGGATGAACGAT**G**AATGTCAATGTGCAAGGAAAAAGAGAATTTTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCAAGCTGATCCTTTTGTGT
 GTGTGCTCCTTGTGTAGGAGAGAAAAAGCTCTATGAAAGAAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTCAATTGACTGCTGGCTGCTTA

FIGURE 202

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSP EARYRLDFG
ESQDWVLEAEDEGE EYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSF
VIDVIDWKTFFQYYPSKDLQRGVLDWKLDFHWEPLPEHV RKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPCMCERLQLQRRLLGCRTPHWF LANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCAEGDILGCPMV LAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQQHWFQENGMI VHI LSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER
```

Signal peptide:

amino acids 1-28

FIGURE 203

GCCTAAGCATGTCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGA
GTCCAGGATGTGGCGCTGCGCTGCTGTGTCCACCTCTCCCTCTCTGTGGCCACTGCTGTGTGTC
TGCCCTCCCAACCGCGCTGCTCAGGGCTTCTTACATCTCCCTCGAACCCACCAGCCCGGCGC
CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCCAACGTCATGTGTGCGTGTGGGAGCGAGC
ACCTCCACCAAGCCGATCTCTCGGGTCCCAAGATCAGTGCGGCAAGTCTGCCTCGGCCTGAGC
CACCCCAAGCCACCATCAGCTTTAGAGAGGGCGGCCCTACATCCCAATACCGCTGGCT
ATCGTGTGGGGTCCCAACGCTGTCTCAGAGGATGAGGGGGACCCCACTCTGCCAATCCCGG
ATTTCTGGCATATGTTTTCAGCCCTCATGGCTCGCAACCCCAACCCCACTCAGAC
CCATGCGAGGTTGAGGATGGGCTTATCTTGAGAGGACCATGCCACCTCGGCCCATTC
CTGTTCGGGGGGCGTGGGGAAGGTGTGGACCCCAAGCTCTATGTCAAAATTACCATTCTCAT
CATCATTTGTTCTGTGGCCACATGTCATCTTCAAGTTCTGTCTGGAGCCGACGCCAGAAGC
GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
GACCTGTCCCGGCTGGAGTCACTGTGCTGGGGCGTCTGGGGACTCACTTACCCCAACCCCT
TGACATGAGGAGCCCGCAGGGGAGCCCGGCTGGATGGCCACCCCAAGGGGGCTCAGC
CCTTCAGATTGAACCGCTCAGGGGACGGGCAATGGGATGGGAGGGCAAGAGGGAAGGCAAC
TTAGGTCTTCAGGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCGAGGCGTTC
CTCCACAGCCCGCTGGCCCTCCCAAGGGGGCTGACAGCAGCTCTCTCTGGGAGGACCCCTTC
CTTCTCCCAAGTCTCTCAGGATCTGTGTCTTATTTCTGTCTGCCCATTAATCCAATCTGCC
TCTTTGGTTTTTTTTCTATGTCACCATGTCTAAGACAACCTTGCCCTTTAACTCTGATTTCCC
CCTCTTTGTCTTGAACCTCCCGTCTATCTTGCCCTACCCCTTGGTTCTGTAGTGTGCCCT
TACCTTTCTCTCTCAGGATTCCTCTGGTGAATCTGTGATGCCCCCAATGTGGGGTGACGC
AAGAGGAGGCCAAGGGGCGGCGCAGACGCCCATCTCCACTGAGGTTGGGCGACTGTGGGA
GCTGGGGCAACAGGGGCTCCTGGCTCCTGCCCTTGCACACCAACCGGAACACTCCCCAGCC
CCAGGGGCAATCCTATCTGCTCGCCCTCTCGAGTGGGGGGCTACATATCTGTGACTCTCG
GGTCCCTGTCCCAACCTTGTGACATACATGAAGACCTTGACACTCACTCCACCTTAC
AGGCCAATTGCAACAGTCTCTGCACCCCTTCCCGCCATACCGCTCCGCTCAGCTGACTCT
CATGTTCTCTGCTTCACGATTTGCACCTCTCCTTCCCAATCTGTGCTCAGCTCACTGAC
TGGTCAGCGTTTCTGCACACTTTTAACTCTCATGTGCGGTTTCCGGGCTGATGTGTGTGGT
TGTGCGGCGTGTCACTCTCTCCTCATGAACACCAACCCACTCGTTTCCGCGACCCCTG
GTGCTGCTCCAGAGGTGGTGGGAGTGAGCTGGGGGCTCCTTGGGCGCTCATCGTCACTG
TCTGTGCCAATCCACACCAATTTGTTTCTGTCTCCCCATCTACTCCAAAGGATGCGCGCA
TCACTCTGAGGCGTCCCCCTTGGGAATGGGGTAGTGAGGCCCGCCAGCTCAACCCAGGCCA
CTGCTAAATCTGTTTCTGCAGAGATGGTTTGGGAGTCCGCTGCTGACTACATGAGAA
AGGAGACCCCAATTGCCCTTCCCTTCTCCTACAGTCCCTTTGTCTGTCTGTCTGTGCTG
TCTGTGTGTGCCATTTCTGTGACTTCAGAGCCCCCTGAGCCAGTCTCCCTCCCTCCAGCT
CCCTTTGGGCGTCCCTTAACCTCACACTAGGCTGCCAGGACCGGAGTCAGTGGTTCAAGGCC
ATCGGAGAGCTGTGCCCTCAAGTCTACCTTCCCTTCCCGAATCCCTCTGTCCTCCCTCTT
CCTCCCTCTCTCTTCCACTCTCTCTCTTTGCTTCCCTGCCCTTTCCCGCTCTCAGTT
CTGCTCTCTCTCTCTACTGTTTTTCCACCTTCTCTCTTCCCTTCTTCCCTGCTTAGGCT
GTGATATATATTTTGTATTAATCTCTCTTCTCTCTTCTGGTGATCATCTTGAATTACTGTG
GGATGTAAGTTTTCAAATTTTCAAATAAGGCTTTGCAAGATAA

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASFPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV
PGRDGSPGANVPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEATIIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCGCTGCCCTCACTCCCGGCCAGG**ATG**
 CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGT^TCTGGCCCTGCGGTG
 CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
 GTCGGGAGAAGGCCCCGTGGAGAGCACCGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
 CAGCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
 GCGGGTCTGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
 CGTGGTGTGGCGCTCGTGGTCGTGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
 GGGGCCGCGCCCGGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA

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FIGURE 206

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPFVESTSPGREPVDTG
FPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GCGCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGGAGCAGCGTCGTTGGTTGGCCGGCGG
 CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
 ACTTCAAGTCCTGCTGGGTGGGCGACATCCCCGTGTGAGGGGCGTGTCTACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCGGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
 CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGAGGG
 ACCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCC
 CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCCTGAAGTTTGTCCATCTCACGCTGGGG
 GTCAACCTGGGGACCCCTTCCCTCCGGCCATGGACACACATACATAAAACCAGGCCGCAT
 CGACTGTGAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG
 ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACCCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGGTCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCCTCCAC
 CTGGCTGTATCGGGTAGGGCGGGGCGGTGGGTTGAGGGGCGCACCACTTCCAAGCCTGTGT
 CCCACAGTCTCTCGGCGCAGTGAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAAC
 TGGCACAAGTAAGTCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
 GGTGAGTATGTGTGGGCGACAGGCTGGCTCCCTCAGCTCCCAGTCTAGAGGGGGTCCCGA
 GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCTTTTCTCCCTCAAAG
 GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTCCCTAAAGGGTCCCCATAGGGTCTGGTTCC
 ACCCATCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCTACGATGGTTAGGGGTGCCCC
 ATGGAGGGGCTGACTGCCCCACATTGCCTTTGAGACAGGACACGAGCATGAGGTAAGGCCGC
 CCTGACCTGGACTTCAGGGGGAGGGGTTAAAGGGAGAGAGAGGGGGGCTAGGGGGTCCCTCT
 AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTAC
 CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCAGCTCCTCTGCCTTCTCCTGG
 CCTGGGACACACAGACCCACCCCGGCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
 AGGGGTGCTCGTAAGCCAACACACGCTGCCGCGCCTGCACACCCTTCGGACATCCCAGGC
 ACGAGGGTGTCTGGAATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGCCT
 GGGGCCCCCAGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
 TGGAAAGTGTCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCCTGCCCCAGGGCAAC
 GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCTACTCTGGAGCTGGGCTGCTGCTGC
 CTCAGGACCCCTCTCCGACCCCGACAGAGCTGAGCTGGCCAGGGCCAGGAGGCGGGAGG
 GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGACAGCTGCGGGA
 TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
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><subunit 1 of 1, 157 aa, 1 stop
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><MW: 17681, pI: 7.65, NX(S/T): 1
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MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI  
PVSGALLTDWSDDTMK  
ELHLAIPAKITREKLDQVATAVYQMDQLYQGKMYFPGYFPNELRNIFRE  
QVHLIQNAIIER  
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLF
```

Signal peptide:

amino acids 1-15

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1  2  3  4  5  6  7  8  9 10 11 12 13 14 15
M A L L L C L V C L T A A L A H G C L H C H S N F S K K F S F Y R H H V N F K S W W V G D I P V S G A L L T D W S D D T M K
E L H L A I P A K I T R E K L D Q V A T A V Y Q M D Q L Y Q G K M Y F P G Y F P N E L R N I F R E Q V H L I Q N A I I E R
H L A P G S W G G G Q L S R E G P S L A P E G S M P S P R G D L F

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FIGURE 209

AGCAGGAGCAGGAGAGGGACAATGGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTCG
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATCCCAGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTTCATCTCTCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTCAAACCTAAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTTGACTTCTCTTGGAACTACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCCTGCCAACACACACACACGACGTGCACACACGACGACGACGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCCTGTCTTAAAAATCTCGTTTTCTC
 TTCTTCTCTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCAATTAATATCAAGT
 TTGTATATGCACATGACTTACACACAACATAGTTCCTGCTCTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAGG
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAATCAACAACCTGCATAATAAATAAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRILDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVVIQHLLIMNKASPEYEENMHRYQKAA
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVSHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGAGCGCGCGTGGAGGTGCCACCCGGCGCGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGTGGCGGCGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTTGGAGTATATACGCCAAAAGAAATCTTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTTTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
 TATATCTGTGATGTCAAAACCCCTCTGCATCGTTGTCCAGCCTGGACACATTAGGCTCTA
 TGTCTGTAAGAAAAGAGAATTTGCCCTGTGTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
 CTGTGGTCTTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACAGTTAAGCAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCCTCTGGATCTCACC
 AGGGCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC
 CTCAGCAAGAAACAAAACCAAACTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
 ACAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
 TGAAAGATGGTATGATTCTACATATGTACCATTTGCTTGTGTTTTGTACTTTCTTTTC
 AGGTCATTTACAATTGGGAGATTTTCAGAAACATTCCTTTCCACCATCATTTAGAAATGGTTTG
 CCTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
 AAAATATGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG
 AAATGTGTCATATCAATTTCTGGATTCAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
 GTCACCTTCACTTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTGGCTT
 GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTA

FIGURE 212

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASININ
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSKINKSESVVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTGCAGCAGTGA CTGCCCGGGCTGCCGGC
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGGC
 TCTCGGCCACGGTGGGTGCGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGGCGCAGTCCCCGCGGCCCCGACCTGAGGGC
 TCGCCTCTGGCCGAGCCGCCACAGAGCAGTCCCTCGCCCCGTGGTCTCCGACAGCCCCGGC
 GCCGCCCTGCTCCAGTGCTTCGCCAGAGCCATCGAGAGAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGCCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAAATTCG
 TCATTTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
 TGAAGAGAAATGTTGCATTTGAGCAAGAAAAAGGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTC AATTGAAT
 CCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
 CTATATGCAGAAAATATTCATGACTTGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
 TGTTTATAAGTAAAAAA

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FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVGVSVSDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTAGCTAAGCTCGGAATTCGGCTCG
AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGCTGCTCCTGC
TCTTGCTGATGGCGGTAGCAGCGCCCACTGAGCCCGGGCAGCGGCTGCCGGGCCGGGACT
GCTGCGCAGGGGCTGGGGCGGAAGTTCGAGAGGGCAGGCTGTGGCACGTTGGGGCTGCT
GCTGGAGCACTCATTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTACTGCTCT
GGAACCAAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
CGACTCCGGGATGTGGCAGCCCTGAATGGCTGTACCGGTCGGATCCCAAGCGCAGCCGG
GGCCCTGGATGGCTGGAAGCTGGTGCTATGTCTCCTCCTTTGTCCCTGCTGCTCCTTG
TGGAGTCGCACCTGTTCGACCAAGCTGACCTGCACGTGGATGTGGCCGGCAACGTGGTGGC
GTGTCGGTGGTGACGCACCCCGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCAAGGCCCTGAGACGCGG
CCTTCATTGAGCGCTGGAGATGGAACAGGCCAGAAAGGCCAAGAACCCCAAGGAGCAGAAG
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCTCTCATGATGTCAGG
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
TTTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTAAAAACATCGACGATACATTGAAATGTG
TGAAGCTTTTGAAGGCTACAGCTTCCAGCAGCCAAAGCAACTGTTGTTTTGGCAAGACGG
TCCTGATGTACAAGCTTGATTGAAATCTACTGCTCACTTGATACGTTATTAGAAACCAAG
GAATGGCTGTCCCATCTCATGTGGCTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
TAAACTGTCCCCAGATCGACAGCAAAAAAAA

FIGURE 216

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGLRLDVAALNGLYRVRIPIRRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSLCCVPPSL

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Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCGGGGCGTCCCGCAGACCGGGGAGCAGGTGTCGGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCTCCTGGCTCCTGCCTGGGGCTGGAAT
 GTCAAGATGCCGGCTAAACCCCTGGAAGGGCTGCAGCAATCCCTCCTTCCCTTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAATCTACCAGCATTACTACTTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGGCTCTACAGTCTCTTTGGCCTAGTGGCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAATCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGCGAGCACTTGGTGGGCTGCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCCTGCGCTGCCTCCTGTGCGACCGCCGC
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTGCTTTCATCTTTGTCTTCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGTGCTGTGCTCATCGTCGCTTCTCTCTTTCATGTTGACTTT
 CTCTACCAGCCAGGCCAGGAGAGTCCGGTGGAGTCTTCATAGCCTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
 CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTTCAGCATTTGCTCTG
 CTGTGATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTGTG
 GACTGACTTTGTGACTGTCTGTGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAAAAA

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FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQAPY
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFNNHVLAVVAG
 VAAEAVASWIGLGPVAPFVAAILLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
 VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSFMASLLGSSLYRIATSKRYHLQ
 PMHLLSLAVLIIVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFSPMSFLRRKVI PET
 EQAGVLNWFVRVPLHSLACLGLLVLDSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA
 ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
 314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGCGGGGCGGCGAGAGGAAACGCGGCGCGGGCGGGCCCGGCCCTGGAG**ATG**
 GTCCCCGCGCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
 CGGCTTCCGTATCCATGATTATTTGTAAGTCTGAGTCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCGCCCGCTGAACCTCCAGAGGCCTGCGGGGAAGTCAAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATT
 CCATCCCAGTCAATGTCACAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGG**TAGA**AAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTACACT
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGTCTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

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Signal peptide:

amino acids 1-20

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[illegible]

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|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
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FIGURE 222

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNnkSSIHCMDLSQRYCLMAVFNVIYLENEDSE
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Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCTTCTGGATGGGGGCCAGGGGGGCCAGGAGAGTATAAAGCGATGTGGAG
 GGTGCCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
 CCATGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
 GGCCCTGGAGGAGGCAAGTATTTGAGCACCACCTGAAGACTACGACCATGAAATCACAGGGCT
 GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG
 ACGTGAAACTGGGAGCCCTTAGGTGGGAATACCCAGGAAGTCACCTGCGAGCCAGGCGAATAC
 ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA
 GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
 AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
 TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
 AGCAAACCTACCCGTGGGTCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
 GTGGTGGTGGCTGATGGTACTGGAGTAAGTACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
 AATAAAGCTTCTGCAGAAA

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FIGURE 224

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQFGEYITKVFAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYANSPPVGR
```

Signal peptide:

amino acids 1-22

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCAGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCTTGGAAAGAAATACATCATGTTTTTCGATAAGAGAAATTTAGGATCCAGTT
 TTTTTTTTAAACGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTGGGATT
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAGAAATAATGTTCCAAAATCGGTCCATCT
 CCAAGGGGTGCAATTTTTCTTCTGGGTGTGAGCGACCCCTGACTCACGTACAGTGCAGCTG
 ACAGGGCTGTCAATGCAACTGGCCCCATAAGCCAAAGCAAAAGCAATAGGACGACCTTTGAA
 CAATACAAAGCATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTACTGACAATGCTTCTTCTGCGCAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGC AAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAAATAGAA
 TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACTTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTTCCAAGACTGCCGCAACC
 TGGAACTTTTGGAGCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACCTTCACTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGAATAAAATCAGTGTCTATAG
 GACAGACCATGCTCTGGACCTGGAGCTCCTTACAAAGCTTGATTATCAGGCCAATGAGATC
 GAAGCTTTCACTGGAGCCAGTGTTTTCCAGTGTGTCGCGAATCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGTCTGGGAATATATGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTG
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCAAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAACCCCTTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACCGCGAGCAGTCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCTGCTGTTATCTACGTGTCTGGAAGCGGTACCCTGCGAGCATGAAGCAG
 CTGACAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAGACAGTCCCTAAAGCAAAT
 GACTCCAGCACCAGGAATTTTATGTAGATTATAAACCCACCAACGAGACCCAGCGAGA
 TGCTGCTGAATGGGACGGGACCTTGACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAGAGCTCTTAAAGCTGGGAAATAAGTGGTGCTTTATTGAACCT
 TGGTGACTATCAAGGGAACGCGATGCCCCCTCCCTTCCCTCTCCCTCTCACTTTTGGTGG
 CAAGATCCTTCTTGTCCGTTTTAGTGCATTCTAATACTGGTCATTTTCTCTCATACATA
 ATCAACCCATTGAATTTAAATACCACAATCAATGTGAAGCTTGAAGCTCCGGTTTAAATATA
 TACCTATTGTAAAGACCTTTACTGATTCCATTAAATGTGCGATTGTTTAAAGATAAAAT
 TCTTTCATAGGTAATAAAAAA

FIGURE 226

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGC PKGRCCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKL LSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNV FAGMIRLKEHL EHNQFSKLN LALFPRLVSLQNL YLQWNKISVIGQTM
SWTWSSLQRDLDSGNEIEAFSGPSVFQCVNLQRLNLD SNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPLPPTVGATEPGPETDADA EHI SFHKIIAGSVALFSLVLI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMPSTQE FVVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
TAAATATGTCAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
AAATTATAATGACCAACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
ATTGATTCTCACAGGCGACCATGGCAGTTTTTGGCTGTTGGAGACTTGGACTCTATTTATGG
GACAGAAGCAGCTGTGAGTCCAACTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTTGA
AAAACAACCTGTATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTTCCA
AAACATCAAATTTAGGAATAGTTATTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
GTCTGAGGAAGGACAATTGACAAAAGAAATGGATGTTGGAAAAATTTTGGTCATGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTTTTTTC
CTAGCATGGGGTCCATAAAAAATTATTATAATTTAAACAATAGCCCAGCCGAGAATCCAACAT
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
CAGCAAAAACAAGAGTTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTTTCTCTGGAGCCTCAGGGCTTG
GCATTATTGTCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
AAACATCAATAGATATCTAAAAA

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDCMVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGAGCTGACGCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCGGCTCAGAAGCTCCGTGGCGGCGGCCGACCGTGACGAGAAGCCC
 ACGGCCAGCTCAGTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCTTTTAACT
 CCTCTTCAAACCTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTTCAAGTCTGTTGTGTTGCTTCTCAGAAATGTTTTTTTA
 CAATCTCAAGAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGATTTTGGACTCATT
 TGGGATTGATGTTACTGCACTATACTTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAAT
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATAT
 TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTGGTGCCAGTAA
 CCACAAATAAAAAGAACGAATGCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTATGGAAC
 TCTAATCTGTACATAAAAAATTTTAAAGTTATTTGTTTGCTTCAGGCAAGCTGTTCAATG
 CTGTACTATGTCCTTAAAGAGAATTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGGATCAAGCTGAAATGAAACACTGAAAACATCGGATT
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA
 TCATTCTGTCATTTGTTCTCAATAGATGTAACGTGTAGACTACGGCTATTTGAAAAATGTG
 CTTATTTGACTATATTTTGTATTCCAAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAAATGTATTGATTTGCACATCCCTTCAGAAATACTGA
 AGGTTAATTATTGTATATTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAATAATAGTT
 GTAACCTCTAATCTTACTTATTGAAGAATAAAGATATTTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTCACATACATGAATGTTCATTTAAAGTTTAATCCTTTGAGTGTCT
 ATGCTATCAGGAAGCACATTTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAAA
 GGTACTTTTGTGCTGCATTAATTTGCTTGGAAGTGTTAAACATTATATTATATAAGAGTATC
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCAATTTATATAATGGCCAC
 TTAATAATAAGAACATTTAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAACCCCTAATCTGGGTAAATTCTAGTATAAAACAAATTAATCTTTAT
 TTAATTTCCCTTGTAAGCAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT
 CTCTATAGTAAGTCTTAAGTGCAGCTAGCTTCTAGATTAGACTATATAGAAATTAGATAT
 TGTATTGTTGCTCATTAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA
 TAAATATGTGAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTCTCTCTCTGTA
 CTGTCTACCTTTATGTGAAGAATTAATTATATGCCATTGCCAGGT

FIGURE 230

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKR TNVSGSIR
```

Important features of the protein:**Signal peptide:**

amino acids 1-26

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 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1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2

FIGURE 231

CGCGGCCGGGCCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCCGTGGCCCTGCTGCTGCTGCGCCGTGAGTGGGGCCAGACAACCCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCTTGGGCCCCACATCATGCCGGTGGCCATCCCTCTGGACACAGCCCA
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGGCT
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTAGTCC
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTCAGAGCCTGCC
 AGCCGAGAGCTTCACCAAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGG
 AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACCTACAGCTGGACCTCTCC
 CACAACCTCATTACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCAACC
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGCCCC
 TGGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGGGGG
 CTGGGAGGCTTACACACCTGTCTCTGGCCAGCTGCAGAGGCTCCCTGAGCTGGCGCCAC
 TGGCTTCCGTGAGCTACCGGGCTGCAAGCTCTGGACCTGTCCGGCAACCCCAAGCTTAACT
 GGGCAGGAGCTGAGGTGTTTTAGGCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC
 AACCTGGTGCCTCTGCTGAGCGCTGCTCCTCACCTCCCGGCACCTGCAGAGCGTCAGCGT
 GGGCAGGATGTGCGGTGCCGGCGCTGGTGGGGAGGGACCTACCCCGGAGGCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCAACC
 ATCTTGT**CGA**CAAAATGGTGGGCCAGGGCCACATACAGACTGCTGTCTGGCTGCCTCAG
 GTCCCGAGTAACCTATGTTCAATGTGCCAACACAGTGGGGAGGCCGAGGCCATGTGGCA
 CGCTCACCACAGGAGTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTACCCCTTTTGTCTACGTTGCTTCCCAAAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAGACTCGGGTCCCTCTCTGCTTCCCTTCCCACTTATCCCCAAGTGCTTCCCTCAT
 GCCTGGGCCGGCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA
 GTTACAGTCCACTGGGCTGAGTGTCCCTTGGGCCCATGGCCAGTCACTCAGGGGCGAGTT
 TCTTTTCTAACAATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCGCTTCATCCTTTCTAT
 TTCCCTAGAACCCTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCTTCTCATGTGAC
 AGATGGGGAACCTGAGGCTTGAGAAGGAAAAAGGCTAATCTAAGTCTCTGCGGGCAGTGGC
 ATGACTGGAGCACAGCCTCTGCCTCCAGCCCGGACCCCAATGCACTTTCTTGTCTCCTCTA
 ATAAGCCCCACCTCCCCGCTGGGCTCCCTTGCTGCCCTTGCTCTGTTCCCAATTAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAACTGGGACTCTGGGCCTCTGACCAGCT
 GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT
 CCAGCCTAGCCAGTTTCTCACCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTACC
 CATTTTCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
 TCTGGCTGGGATCTCCAAGGGCCTCTTGATTCAGTCCCACTGGCCCTGAGCAGCAGCAGC
 CCTTCTTACCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCATGTCTATGC
 TCTACCCCGAGGCGAGCATCTCAGCTCCGAACCTTGGGCTGTTTCTTAGTCTTCATTTTA
 TAAAAGTTGTTGCCTTTTTAAACGAGTGTCACTTTCAACCGGCTCCCTACCCCTGCTGGC
 CGGGGATGGAGACATGTCAATTTGTAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAT
 ATTTGCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
 AGGGGCTGGCCCCACAGACCCCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGGCCTAGC
 CATCATCTATCTAACCGTCTTGATTTAATAAACACTATAAAGGTTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MFWPLLLLLLAVSGAQTTTRPCFPGCQCEVETFGLEFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVFLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCTCCCCAGTTCCTCTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATCCCCA
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACCTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCAC
 GGGAGGCTTGGCAGTTTTTCTTACTCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGGCTCGCCAAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTTCAGGCT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTGCAGTGATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGATAAGATTTTGTAAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT
 ATTTTTTTTACTTGGACATGAACTTTAAAAAAATTACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTATACAGTAAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT
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 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTGTATGTGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAAATTGTGTAT
 CTTCAGCCAGGAATCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

1-16
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 49-64
 65-80
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 353-368
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 385-400
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 417-432
 433-448
 449-464
 465-480
 481-496
 497-512
 513-528
 529-544
 545-560
 561-576
 577-592
 593-608
 609-624
 625-640
 641-656
 657-672
 673-688
 689-704
 705-720
 721-736
 737-752
 753-768
 769-784
 785-800
 801-816
 817-832
 833-848
 849-864
 865-880
 881-896
 897-912
 913-928
 929-944
 945-960
 961-976
 977-992
 993-1008
 1009-1024
 1025-1040
 1041-1056
 1057-1072
 1073-1088
 1089-1104
 1105-1120
 1121-1136
 1137-1152
 1153-1168
 1169-1184
 1185-1200
 1201-1216
 1217-1232
 1233-1248
 1249-1264
 1265-1280
 1281-1296
 1297-1312
 1313-1328
 1329-1344
 1345-1360
 1361-1376
 1377-1392
 1393-1408
 1409-1424
 1425-1440
 1441-1456
 1457-1472
 1473-1488
 1489-1504
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 1585-1600
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 1617-1632
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 1857-1872
 1873-1888
 1889-1904
 1905-1920
 1921-1936
 1937-1952
 1953-1968
 1969-1984
 1985-2000

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
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EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLK'ITNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLTIKKDLRLSHAHMTCHCGEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGGCGCTACTGCTGAATGTCCGTCGCCGAGGAGGAGGAGAGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAAT
 GGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGCGATTTTCGTGGTGACATCATGCATTTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAACACTACTTGGT
 ATTGAATACACCCTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGCTGAGAATGACCC
 CTGCGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

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FIGURE 236

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
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RESAPYRGMVRTALGIIEEGFLKLWQGVTPATYRHVVYSGGRMVTYEHLREVVFVGKSEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGGGACGCCGCGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
 TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGATCCTAAGCCAGAACAGTTGAACCATGCCTT
 TCACACATGTGGTGATTTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGCGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA
 TATTTTTTAGCACCTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
 TTCTTAAGTCACATTTTCCTTTTGTTATATCTGTTTGTAGATAGGTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTCTTTACATTTTTATGTTT
 TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG
 CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
 AAAAATACAAAAATTAGCCAGGCATGGTGGTGGTGCTGTAATCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAAATCGCTTGAACCCGGGGGCGAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
 TGCATCTAGCCTGGGGGAGAAAGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTTACGAAGTTGTAACTTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
 AAAATATTTGTTCTTATGTATTGAAGAAGTGTACTTTTATATAATGATTTTTTAAATGCC
 AAAGGACTAGTTTGAAAGCTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFTCG
 VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
 NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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FIGURE 239

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCCAGGGTGGT
 GGTCAGCTGGGTAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAGCTGACCCCAGCCACCTTCACCTGGACAG
GATGAGAGTGTACGGTGTGCTTCGGCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTATTATCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCAACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCCTGGTGTCTGGTGG
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 GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCTTTGAGCAGTTCCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTT**TAG**GGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCCTCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGTCTTCTGTCAGGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTA
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 3%
 2%
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FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
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ANYFAFKICSGAANVVGFTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDNTNKYEGWPELLEMEGCMPPKPF
```

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCTTGGGGAT
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCTTGGAGGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCAGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCTCCTCTCTCTCTGCTGTCTTAGTCTCTAGTCTCAAATCCCAGTCCC
 CTGCACCCCTTCTCTGGGACACTATGTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCCTGAGTGTGGAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
 GACATTTGACCCTGATTTGCCTGCTGCGAGCCACGGATATGACCAGCCTGGCACCAGAGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGTGTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCGATGAAGTCAGGCATAAAGATCAGAAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAGCCACGACTGAGGCATTAAATTCCTTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCAATTCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAATCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA
 TACTGCGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA
 TATTGGAAATTAAAGTTTCTGACTTT

FIGURE 242

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>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTDFDPLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTI
FSTEEEPSKLLVQNYRALQPLNQRMVFAFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

[illegible]

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLPDQGTLPNQQQSNQVFPSLSLIPLTQM
 LTLGPDHLHLNPAAGMTFGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
 LPQIIFTSIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTTPAGRLPTPSG
 TDDDFAVTTPAGIQRSTHAI EEATTESANGIQ

Signal peptide:

amino acids 1-16

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FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCCCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGGCCATGCGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCCTCC
 TGCTGCTCTGCTGCTGTCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCTGGTCGAGACGGGAGCCCTGGGGCCAATGTATTCGGGGTACACCTG
 GGATCCCAGGTGCGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG
 GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGATACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
 CCTGAAATGAATTCACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGTGGATTAGTGGATGTTGCTATCTGGTGGCACTTGTTTCAGATTACCCAAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTTATGAAGAAGTACCCAAAATA
ATAGCTTTAATTTTCATTTGCTACCTCTTTTTTTATATGCCTTGGAATGGTTCACTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGT
 GGTTCATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTGGAATATTTGTGTGGTCTTTTGTTTTTCTCTTAGTATAGCATTTTTAAAAAATA
 TAAAAGCTACCAATCTTTGTACAATTTGTAATGTTAAGAATTTTTTTTATATCTGTTAAAT
 AAAAATTATTTCCAACA

FIGURE 246

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
```

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAA SPQR LRLGL LLLLLL LQLPAPSSASE I PKGKQKAQLRQREVVDLYNGMCLQGPAVG
PGRDGSPGANV I PGTPGI PRDGF KGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLKGIA
ECTFTKMRSNALSRLVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAI IYLDQGSPEMN
STINIHR TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDA STGWNVSVSRII I EELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

| code | name | code | name | code | name |
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